GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 11, 2004, 04:01:33 ; Search time 3521 Seconds
(without alignments)
6339.318 Million cell updates/sec

Title: US-10-045-116-1
Perfect score: 472
Sequence: 1 AGCCACCACCCAGTGAGCCT.....ACGTTCCTGGAACTCAAGCA 472

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
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9: gb_pr:*
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11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	472	100.0	472	6	BD195486	BD195486 Adenoviru
2	472	100.0	472	6	BD195520	BD195520 Adenoviru
3	472	100.0	472	6	AR451687	AR451687 Sequence
4	472	100.0	472	6	AR451733	AR451733 Sequence
5	471	99.8	3500	6	AX705342	AX705342 Sequence
6	471	99.8	11288	6	AR134885	AR134885 Sequence
7	471	99.8	11288	6	AR182304	AR182304 Sequence
8	471	99.8	11288	6	AR370519	AR370519 Sequence
9	471	99.8	11288	6	AR479027	AR479027 Sequence
10	471	99.8	11288	6	AX269130	AX269130 Sequence
11	471	99.8	11288	9	HSCRCANTA	Z21818 H.sapiens c
12	471	99.8	15056	6	BD195539	BD195539 Adenoviru
13	471	99.8	15056	6	BD224258	BD224258 Adenoviru
14	471	99.8	15056	6	AR266427	AR266427 Sequence
15	471	99.8	15056	6	AR474484	AR474484 Sequence
16	471	99.8	15056	6	AX259954	AX259954 Sequence
17	471	99.8	15056	6	AX262359	AX262359 Sequence
18	471	99.8	39707	9	AC008999	AC008999 Homo sapi
19	455.8	96.6	4137	9	HSCEATG	X62151 H.sapiens c
20	455.8	96.6	4138	6	AX822164	AX822164 Sequence
21	455.8	96.6	4138	6	AX825804	AX825804 Sequence
22	432.4	91.6	3281	6	A37261	A37261 Sequence 1
23	432.4	91.6	3281	9	HUMCEA01	M59255 Human carci
24	278.2	58.9	3500	6	AX705383	AX705383 Sequence
25	271.8	57.6	3500	6	AX705405	AX705405 Sequence
26	266.2	56.4	4138	6	AX822351	AX822351 Sequence
27	266.2	56.4	4138	6	AX825991	AX825991 Sequence
28	264.8	56.1	645	9	HSCGM2PRO	X98312 H.sapiens c
c 29	263.2	55.8	39753	9	AC005797	AC005797 Homo sapi
c 30	263	55.7	3500	6	AX705384	AX705384 Sequence
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32	259.8	55.0	4138	6	AX826119	AX826119 Sequence
c 33	256.6	54.4	3500	6	AX705406	AX705406 Sequence
c 34	247.8	52.5	4138	6	AX822352	AX822352 Sequence
c 35	247.8	52.5	4138	6	AX825992	AX825992 Sequence
c 36	241.4	51.1	4138	6	AX822480	AX822480 Sequence
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c 42	134	28.4	38235	9	AC004559	AC004559 Homo sapi
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c 44	120.8	25.6	39801	9	AC005955	AC005955 Homo sapi
c 45	120.8	25.6	44332	9	AC005794	AC005794 Homo sapi

ALIGNMENTS

RESULT 1
BD195486
LOCUS BD195486 472 bp DNA linear PAT 17-JUL-2003
DEFINITION Adenovirus vectors containing heterologous transcription regulatory elements and methods of using same.
ACCESSION BD195486
VERSION BD195486.1 GI:33005256
KEYWORDS JP 2002514074-A/7.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 472)
AUTHORS Henderson,D.R., Yu,D.C. and Lamparski,H.G.
TITLE Adenovirus vectors containing heterologous transcription regulatory elements and methods of using same
JOURNAL Patent: JP 2002514074-A 7 14-MAY-2002;
CALYDON INC
COMMENT OS Unidentified
PN JP 2002514074-A/7
PD 14-MAY-2002
PF 03-MAR-1998 JP 1998538674
PR 03-MAR-1997 US 60/039762,03-MAR-1997 US 60/039763 PR 04-AUG-1997 US 60/054523,02-MAR-1998 US 09/033556 PI DANIEL R HENDERSON,DE CHAO YU,HENRY G LAMPARSKI PC
C12N15/86,C12N5/10,A61K48/00,A61K47/48,C12N11/08 CC Strandedness: Single;
CC Topology: Linear;
CC Adenovirus vectors containing heterologous transcription CC regulatory
CC elements and methods of using same
FH Key Location/Qualifiers
FT source 1. .472
FT /organism='Unidentified'.
FEATURES Location/Qualifiers
source 1. .472
/organism="unidentified"
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/db_xref="taxon:32644"
ORIGIN

Query Match 100.0%; Score 472; DB 6; Length 472;
Best Local Similarity 100.0%; Pred. No. 5.8e-143;

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Qy         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
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Db         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120

Qy        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
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Db        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180

Qy        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240
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Qy        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300
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Qy        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360
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Db        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360

Qy        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
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Db        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420

Qy        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGCA 472
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RESULT 2
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LOCUS       BD195520                472 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Adenovirus vectors specific for cells expressing carcinoembryonic
            antigens and methods of use thereof.
ACCESSION   BD195520
VERSION     BD195520.1  GI:33005290
KEYWORDS    JP 2002514075-A/1.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 472)
  AUTHORS   Lamparski,H.G., Henderson,D.R. and Schuur,E.R.
  TITLE     Adenovirus vectors specific for cells expressing carcinoembryonic
            antigens and methods of use thereof
  JOURNAL   Patent: JP 2002514075-A 1 14-MAY-2002;
            CALYDON INC
COMMENT     OS   Unidentified
            PN   JP 2002514075-A/1
            PD   14-MAY-2002
            PF   03-MAR-1998 JP 1998538697
            PR   03-MAR-1997 US    60/039763,02-MAR-1998 US    60/039763 PI
            HENRY G LAMPARSKI,DANIEL R HENDERSON,ERIC R SCHUUR PC
            C12N15/86,C12N5/10,A61K48/00,A61K47/48,C12Q1/70,C12N11/08 CC
            Strandedness: Double;
            CC   Topology: Linear;
            CC   Adenovirus vectors specific for cells expressing  CC
             carcinoembryonic antigens
            CC   and methods of use thereof
            FH   Key             Location/Qualifiers
            FT   source          1. .472
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
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                     /organism="unidentified"
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                     /db_xref="taxon:32644"
ORIGIN

  Query Match           100.0%;  Score 472;  DB 6;  Length 472;
  Best Local Similarity   100.0%;  Pred. No. 5.8e-143;
  Matches  472;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
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Db          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60

Qy         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
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Qy        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
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Db        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180

Qy        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240
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Db        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240

Qy        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300
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Db        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300

Qy        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360
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Db        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360

Qy        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
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Qy        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGCA 472
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Db        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGCA 472


RESULT 3
AR451687
LOCUS       AR451687                472 bp    DNA     linear   PAT 20-FEB-2004
DEFINITION  Sequence 7 from patent US 6676935.
ACCESSION   AR451687
VERSION     AR451687.1  GI:42682802
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 472)
  AUTHORS   Henderson,D.R. and Schuur,E.R.
  TITLE     Tissue specific adenoviral vectors
  JOURNAL   Patent: US 6676935-A 7 13-JAN-2004;
FEATURES             Location/Qualifiers
     source          1. .472
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ORIGIN

  Query Match           100.0%;  Score 472;  DB 6;  Length 472;
  Best Local Similarity   100.0%;  Pred. No. 5.8e-143;
  Matches  472;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
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Qy         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
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Qy        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
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Db        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
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Qy        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240
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Db        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240

Qy        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300
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Qy        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360
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Qy        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
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Qy        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGCA 472
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RESULT 4
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LOCUS       AR451733                472 bp    DNA     linear   PAT 20-FEB-2004
DEFINITION  Sequence 54 from patent US 6676935.
ACCESSION   AR451733
VERSION     AR451733.1  GI:42682848
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 472)
  AUTHORS   Henderson,D.R. and Schuur,E.R.
  TITLE     Tissue specific adenoviral vectors
  JOURNAL   Patent: US 6676935-A 54 13-JAN-2004;
FEATURES             Location/Qualifiers
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ORIGIN

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Qy          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
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Qy         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
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Qy        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
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Db        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180

Qy        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240
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Db        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240

Qy        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300
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Db        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300

Qy        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360
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Qy        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
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RESULT 5
AX705342
LOCUS       AX705342                3500 bp    DNA     linear   PAT 04-APR-2003
DEFINITION  Sequence 11 from Patent WO03014388.
ACCESSION   AX705342
VERSION     AX705342.1  GI:29562007
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Distler,J., Model,F. and Taubert,H.
  TITLE     Method and nucleic acids for the analysis of colon cancer
  JOURNAL   Patent: WO 03014388-A 11 20-FEB-2003;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .3500
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ORIGIN

  Query Match             99.8%;  Score 471;  DB 6;  Length 3500;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-142;
  Matches  471;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
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Db       2566 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 2625

Qy        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
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Qy        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240
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Db       2926 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 2976


RESULT 6
AR134885
LOCUS       AR134885                11288 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 1 from patent US 6194211.
ACCESSION   AR134885
VERSION     AR134885.1  GI:14123790
KEYWORDS    .
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SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11288)
  AUTHORS   Richards,C.Ann. and Huber,B.
  TITLE     Transcriptional regulatory sequence of carcinoembryonic antigen for
            expression targeting
  JOURNAL   Patent: US 6194211-A 1 27-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .11288
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             99.8%;  Score 471;  DB 6;  Length 11288;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-142;
  Matches  471;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
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Qy         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10354 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 10413

Qy        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10414 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 10473

Qy        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10474 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 10533

Qy        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10534 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 10593

Qy        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10594 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 10653

Qy        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10654 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 10713

Qy        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10714 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 10764


RESULT 7
AR182304
LOCUS       AR182304               11288 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 4 from patent US 6337209.
ACCESSION   AR182304
VERSION     AR182304.1  GI:20225220
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11288)
  AUTHORS   Huber,B. and Richards,C.A.
  TITLE     Molecular constructs containing a carcinoembryonic antigen
            regulatory sequence
  JOURNAL   Patent: US 6337209-A 4 08-JAN-2002;
FEATURES             Location/Qualifiers
     source          1. .11288
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             99.8%;  Score 471;  DB 6;  Length 11288;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-142;
  Matches  471;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10294 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 10353

Qy         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10354 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 10413

Qy        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10414 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 10473

Qy        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10474 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 10533

Qy        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10534 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 10593

Qy        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10594 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 10653

Qy        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10654 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 10713

Qy        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10714 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 10764


RESULT 8
AR370519
LOCUS       AR370519               11288 bp    DNA     linear   PAT 12-SEP-2003
DEFINITION  Sequence 4 from patent US 6300490.
ACCESSION   AR370519
VERSION     AR370519.1  GI:34607246
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11288)
  AUTHORS   Huber,B., Richards,C.A. and Austin,E.A.
  TITLE     Molecular constructs comprising a carcinoembryonic antigen (CEA)
            transcriptional regulatory region
  JOURNAL   Patent: US 6300490-A 4 09-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .11288
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             99.8%;  Score 471;  DB 6;  Length 11288;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-142;
  Matches  471;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10294 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 10353

Qy         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10354 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 10413

Qy        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10414 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 10473
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Qy        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10474 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 10533

Qy        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10534 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 10593

Qy        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10594 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 10653

Qy        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10654 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 10713

Qy        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10714 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 10764


RESULT 9
AR479027
LOCUS       AR479027               11288 bp    DNA     linear   PAT 14-MAY-2004
DEFINITION  Sequence 4 from patent US 6699690.
ACCESSION   AR479027
VERSION     AR479027.1  GI:47237926
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11288)
  AUTHORS   Huber,B. and Richards,C.A.
  TITLE     Molecular constructs with a carcinoembryonic antigen (CEA)
            transcriptional regulatory sequence
  JOURNAL   Patent: US 6699690-A 4 02-MAR-2004;
FEATURES             Location/Qualifiers
     source          1. .11288
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             99.8%;  Score 471;  DB 6;  Length 11288;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-142;
  Matches  471;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10294 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 10353

Qy         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10354 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 10413

Qy        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10414 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 10473

Qy        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10474 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 10533

Qy        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10534 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 10593

Qy        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10594 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 10653

Qy        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10654 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 10713

Qy        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10714 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 10764


RESULT 10
AX269130
LOCUS       AX269130               11288 bp    DNA     linear   PAT 29-OCT-2001
DEFINITION  Sequence 1 from Patent WO0174861.
ACCESSION   AX269130
VERSION     AX269130.1  GI:16542049
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Vile,R.G., Harrington,K., Murphy,S. and Bateman,A.
  TITLE     Compositions and methods for tissue specific gene regulation
            therapy
  JOURNAL   Patent: WO 0174861-A 1 11-OCT-2001;
            MAYO FOUNDATION FOR MEDICAL EDUCATION AND RESEARCH (US)
FEATURES             Location/Qualifiers
     source          1. .11288
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
     CDS             10804. .10938
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAD10314.1"
                     /db_xref="GI:16542050"
                     /translation="MESPSAPPHRWCIPWQRLLLTGEGRTTWERVGGGSWGLLGRTGL
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ORIGIN

  Query Match             99.8%;  Score 471;  DB 6;  Length 11288;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-142;
  Matches  471;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10294 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 10353

Qy         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10354 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 10413

Qy        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10414 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 10473

Qy        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10474 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 10533

Qy        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10534 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 10593

Qy        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10594 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 10653

Qy        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10654 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 10713

Qy        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10714 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 10764
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RESULT 11
HSCRCANTA
LOCUS       HSCRCANTA              11288 bp    DNA     linear   PRI 29-MAY-1996
DEFINITION  H.sapiens carcinoembryonic antigen gene.
ACCESSION   Z21818
VERSION     Z21818.1  GI:437783
KEYWORDS    carcinoembryonic antigen.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Schrewe,H., Thompson,J., Bona,M., Hefta,L.J., Maruya,A.,
            Hassauer,M., Shively,J.E., von Kleist,S. and Zimmermann,W.
  TITLE     Cloning of the complete gene for carcinoembryonic antigen: analysis
            of its promoter indicates a region conveying cell type-specific
            expression
  JOURNAL   Mol. Cell. Biol. 10 (6), 2738-2748 (1990)
  MEDLINE   90258861
   PUBMED   2342461
  REMARK    (sites)
REFERENCE   2  (bases 1 to 11288)
  AUTHORS   Richards,C.A., Wolberg,A.S. and Huber,B.E.
  TITLE     The transcriptional control region of the human carcinoembryonic
            antigen gene: DNA sequence and homology studies
  JOURNAL   DNA Seq. 4 (3), 185-196 (1993)
  MEDLINE   94214170
   PUBMED   8161821
REFERENCE   3  (bases 1 to 11288)
  AUTHORS   Richards,C.A., Austin,E.A. and Huber,B.E.
  TITLE     Transcriptional regulatory sequences of carcinoembryonic antigen:
            identification and use with cytosine deaminase for tumor-specific
            gene therapy
  JOURNAL   Hum. Gene Ther. 6 (7), 881-893 (1995)
  MEDLINE   96097131
   PUBMED   7578407
REFERENCE   4  (bases 1 to 11288)
  AUTHORS   Richards,C.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-FEB-1993) Richards C. A., Burroughs Wellcome Co.,
            Cell Biology, 3030 Cornwallis Rd, Research Triangle Park, North
            Carolina, USA, 27709
COMMENT     Overlapping sequence: U17131.
FEATURES             Location/Qualifiers
     source          1. .11288
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="19"
                     /clone="lambdaCEA1"
                     /clone_lib="library LL19NL01 from ATCC"
                     /germline
     repeat_region   520. .857
                     /citation=[2]
                     /rpt_family="Alu"
                     /rpt_type=DISPERSED
     repeat_region   2106. .2155
                     /citation=[2]
                     /rpt_family="CA"
                     /rpt_type=TANDEM
                     /rpt_unit="2106. .2107"
     repeat_region   2308. .2501
                     /citation=[2]
                     /rpt_type=TANDEM
                     /rpt_unit="2344. .2379"
     repeat_region   6746. .6887
                     /citation=[2]
                     /rpt_family="Alu"
                     /rpt_type=DISPERSED
     mRNA            10694. .11288
                     /citation=[1]
     exon            10694. .10867
                     /citation=[1]
     CDS             10804. .10938
                     /citation=[1]
                     /codon_start=1
                     /product="carcinoembryonic antigen"
                     /protein_id="CAA79884.1"
                     /db_xref="GI:437784"
                     /db_xref="GOA:Q14081"
                     /db_xref="TrEMBL:Q14081"
                     /translation="MESPSAPPHRWCIPWQRLLLTGEGRTTWERVGGGSWGLLGRTGL
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     intron          10868. .11288
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ORIGIN

  Query Match           99.8%;  Score 471;  DB 9;  Length 11288;
  Best Local Similarity  100.0%;  Pred. No. 1.9e-142;
  Matches  471;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10294 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 10353

Qy         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10354 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 10413

Qy        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10414 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 10473

Qy        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10474 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 10533

Qy        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10534 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 10593

Qy        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10594 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 10653

Qy        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10654 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 10713

Qy        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10714 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 10764


RESULT 12
BD195539
LOCUS       BD195539               15056 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Adenovirus vectors specific for cells expressing carcinoembryonic
            antigens and methods of use thereof.
ACCESSION   BD195539
VERSION     BD195539.1  GI:33005309
KEYWORDS    JP 2002514075-A/20.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 15056)
  AUTHORS   Lamparski,H.G., Henderson,D.R. and Schuur,E.R.
  TITLE     Adenovirus vectors specific for cells expressing carcinoembryonic
            antigens and methods of use thereof
  JOURNAL   Patent: JP 2002514075-A 20 14-MAY-2002;
            CALYDON INC
COMMENT     OS   Unidentified
            PN   JP 2002514075-A/20
            PD   14-MAY-2002
            PF   03-MAR-1998 JP 1998538697
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            PR   03-MAR-1997 US    60/039763,02-MAR-1998 US    60/039763 PI
            HENRY G LAMPARSKI,DANIEL R HENDERSON,ERIC R SCHUUR PC
            C12N15/86,C12N5/10,A61K48/00,A61K47/48,C12Q1/70,C12N11/08 CC
            Strandedness: Single;
            CC   Topology: Linear;
            CC   Adenovirus vectors specific for cells expressing  CC
             carcinoembryonic antigens
            CC   and methods of use thereof
            FH   Key             Location/Qualifiers
            FT   source          1. .15056
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .15056
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match             99.8%;  Score 471;  DB 6;  Length 15056;
  Best Local Similarity   100.0%;  Pred. No. 2e-142;
  Matches  471;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14062 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 14121

Qy         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
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Db      14122 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 14181

Qy        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
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Db      14182 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 14241

Qy        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14242 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 14301

Qy        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300
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Db      14302 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 14361

Qy        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14362 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 14421

Qy        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14422 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 14481

Qy        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 471
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Db      14482 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 14532


RESULT 13
BD224258
LOCUS       BD224258               15056 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Adenovirus vectors containing cell status-specific response
            elements and methods of use thereof.
ACCESSION   BD224258
VERSION     BD224258.1  GI:33034028
KEYWORDS    JP 2002525063-A/4.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 15056)
  AUTHORS   Yu,D.C. and Henderson,D.R.
  TITLE     Adenovirus vectors containing cell status-specific response
            elements and methods of use thereof
  JOURNAL   Patent: JP 2002525063-A 4 13-AUG-2002;
            CALYDON INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002525063-A/4
            PD   13-AUG-2002
            PF   10-SEP-1999 JP 2000570347
            PR   10-SEP-1998 US    60/099791,09-SEP-1999 US    09/392822 PI
            DE CHAO YU,DANIEL R HENDERSON
            PC
            C12N15/09,A61K48/00,A61P35/00,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
             10,
            PC   C12N7/02//A61K35/76,C12N15/00,C12N5/00
            CC   Adenovirus vectors containing cell status-specific response
            CC            elements and
            CC   methods of use thereof
            FH   Key             Location/Qualifiers
            FT   source          1. .15056
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             99.8%;  Score 471;  DB 6;  Length 15056;
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  Matches  471;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14062 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 14121

Qy         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
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Db      14122 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 14181

Qy        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
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Db      14182 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 14241

Qy        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14242 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 14301

Qy        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14302 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 14361

Qy        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14362 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 14421

Qy        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14422 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 14481

Qy        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14482 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 14532


RESULT 14
AR266427
LOCUS       AR266427               15056 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 10 from patent US 6495130.
ACCESSION   AR266427
VERSION     AR266427.1  GI:29695383
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15056)
  AUTHORS   Henderson,D.R. and Yu,D.C.
  TITLE     Target cell-specific adenoviral vectors containing E3 and methods
```

```
          of use thereof
  JOURNAL   Patent: US 6495130-A 10 17-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .15056
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             99.8%;  Score 471;  DB 6;  Length 15056;
  Best Local Similarity   100.0%;  Pred. No. 2e-142;
  Matches  471;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
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Db      14062 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 14121

Qy         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
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Db      14122 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 14181

Qy        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14182 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 14241

Qy        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14242 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 14301

Qy        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14302 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 14361

Qy        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14362 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 14421

Qy        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14422 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 14481

Qy        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14482 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 14532


RESULT 15
AR474484
LOCUS       AR474484               15056 bp    DNA     linear   PAT 20-FEB-2004
DEFINITION  Sequence 14 from patent US 6692736.
ACCESSION   AR474484
VERSION     AR474484.1  GI:42713365
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15056)
  AUTHORS   Yu,D.-C., Li,Y., Little,A.S. and Henderson,D.R.
  TITLE     Cell-specific adenovirus vectors comprising an internal ribosome
            entry site
  JOURNAL   Patent: US 6692736-A 14 17-FEB-2004;
FEATURES             Location/Qualifiers
     source          1. .15056
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             99.8%;  Score 471;  DB 6;  Length 15056;
  Best Local Similarity   100.0%;  Pred. No. 2e-142;
  Matches  471;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14062 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 14121

Qy         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14122 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 14181

Qy        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14182 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 14241

Qy        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14242 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 14301

Qy        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300
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Db      14302 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 14361

Qy        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360
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Db      14362 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 14421

Qy        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
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Db      14422 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 14481

Qy        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14482 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 14532

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Job time : 3523 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 11, 2004, 03:58:23 ; Search time 428 Seconds
(without alignments)
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Title: US-10-045-116-1
Perfect score: 472
Sequence: 1 AGCCACCACCCAGTGAGCCT.....ACGTTCCTGGAACTCAAGCA 472

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	472	100.0	472	2	AAV52944	Aav52944 CEA trans
2	472	100.0	472	12	ADI36414	Adi36414 Human car
3	472	100.0	472	12	ADI36390	Adi36390 Human car
4	471	99.8	3500	8	ACF62762	Acf62762 Human CEA
5	471	99.8	11288	2	AAQ90512	Aaq90512 CEA clone
6	471	99.8	11288	5	AAS14778	Aas14778 Human car
7	471	99.8	15056	2	AAV52967	Aav52967 Carcinoem
8	471	99.8	15056	3	AAZ99933	Aaz99933 DNA seque
9	471	99.8	15056	3	AAA46851	Aaa46851 Nucleotid
10	471	99.8	15056	5	AAH43620	Aah43620 CEA-TRE.
11	471	99.8	15056	5	AAF87238	Aaf87238 CEA-TRE f
12	471	99.8	15056	6	ABK99582	Abk99582 Prostate-
13	471	99.8	15056	8	ACD07309	Acd07309 Human car
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15	432.4	91.6	3281	10	ADC37109	Adc37109 DNA of a
16	359	76.1	14556	2	AAQ90511	Aaq90511 CEA genom
17	350.4	74.2	425	8	ACC47273	Acc47273 hTERT gen
18	278.2	58.9	3500	8	ACF62803	Acf62803 Colon can
19	271.8	57.6	3500	8	ACF62825	Acf62825 Colon can
20	266.2	56.4	4138	10	ADB54187	Adb54187 Pretreate
c 21	263	55.7	3500	8	ACF62804	Acf62804 Colon can
22	259.8	55.0	4138	10	ADB54315	Adb54315 Pretreate
c 23	256.6	54.4	3500	8	ACF62826	Acf62826 Colon can
c 24	247.8	52.5	4138	10	ADB54188	Adb54188 Pretreate
c 25	241.4	51.1	4138	10	ADB54316	Adb54316 Pretreate
26	225	47.7	271	2	AAZ09584	Aaz09584 Carcinoem
c 27	120.8	25.6	39801	6	ABK83462	Abk83462 Human cDN
28	94	19.9	3774	2	AAQ73990	Aaq73990 CEA clone
29	85.8	18.2	39801	6	ABK83462	Abk83462 Human cDN
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38	75	15.9	2974	10	ADD25525	Add25525 Binding d
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40	75	15.9	2974	12	ADM32425	Adm32425 Human can
41	75	15.9	2974	12	ADM72830	Adm72830 Human CEA
42	75	15.9	2974	12	ADO28644	Ado28644 Human CEA
43	75	15.9	2975	6	ABQ82535	Abq82535 Human CEA
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45	67.8	14.4	2547	5	ADL62109	Adl62109 Human ova

ALIGNMENTS

RESULT 1
AAV52944
ID AAV52944 standard; DNA; 472 BP.
XX
AC AAV52944;
XX
DT 21-DEC-1998 (first entry)
XX
DE CEA transcriptional regulatory element (CEA-TRE).
XX
KW Carcinoembryonic antigen; transcriptional regulatory element; CEA-TRE;
KW human; promoter; enhancer; adenovirus; vector; cancer; gene therapy; ds.
XX
OS Homo sapiens.
XX
PN WO9839467-A2.
XX
PD 11-SEP-1998.
XX
PF 03-MAR-1998; 98WO-US004133.
XX
PR 03-MAR-1997; 97US-0039763P.
PR 02-MAR-1998; 98US-00033555.
XX
PA (CALY-) CALYDON INC.
XX
PI Lamparski HG, Henerson DR, Schuur ER;
XX
DR WPI; 1998-495862/42.
XX
PT New adenovirus vectors, particularly for cancer therapy - comprising
PT adenovirus gene under transcriptional control of carcinoembryonic antigen
PT transcriptional regulatory element.
XX
PS Claim 13; Page 62-63; 95pp; English.
XX
CC This 472 nucleotide fragment comprises nucleotides -402 to +69 of the
CC human carcinoembryonic antigen transcriptional regulatory element (CEA-
CC TRE). It was isolated from human genomic DNA by PCR (see AAV52945-46).
CC The CEA-TRE is capable of mediating gene expression specific to cells
CC capable of expressing CEA or capable of CRE-TRE-mediated transcription. A
CC claimed replication-competent adenovirus (Ad) vector comprises an Ad gene
CC under transcriptional control of a CEA-TRE. Also claimed are: (1) a host
CC cell transformed with a Ad vector as above; (2) a method of making a

```
CC   masked Ad, and (3) an Ad complexed with a masking agent. By providing for
CC   transcriptional initiating regulation dependent upon CEA expression,
CC   virus replication can be restricted to target cells which allow a CEA-TRE
CC   to function, particularly carcinoma cells expressing CEA. The vectors can
CC   be used to detect and monitor samples for the presence of cells that
CC   allow a CEA-TRE to function, and to selectively kill such cells,
CC   especially malignant cells. Preferred vectors contain a CEA-TRE
CC   comprising nucleotides 313-472 or 104-472 of the 472 nucleotide fragment,
CC   especially comprising an enhancer and/or a promoter of the CEA gene
XX
SQ   Sequence 472 BP; 142 A; 125 C; 134 G; 71 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 472;  DB 2;  Length 472;
  Best Local Similarity  100.0%;  Pred. No. 1.6e-126;
  Matches  472;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120

Qy        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
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Db        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180

Qy        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240
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Db        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240

Qy        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300
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Qy        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360
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Qy        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
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Db        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420

Qy        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGCA 472
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGCA 472


RESULT 2
ADI36414
ID   ADI36414 standard; DNA; 472 BP.
XX
AC   ADI36414;
XX
DT   22-APR-2004  (first entry)
XX
DE   Human carcinoembryonic antigen transposon response element DNA SeqID7.
XX
KW   ds; carcinoembryonic antigen; CEA; human; prostate;
KW   transcriptional response element; TRE; polyethylene glycol; PEG;
KW   masking agent; tumour cell growth; proliferation; psoriatic lesion;
KW   wound healing; hyperplasia; cancer; cytostatic; antipsoriatic; vulnerary.
XX
OS   Homo sapiens.
XX
PN   US2003152553-A1.
XX
PD   14-AUG-2003.
XX
PF   02-MAY-2002; 2002US-00139089.
XX
PR   27-JUN-1995;   95US-00495034.
PR   26-JUN-1996;   96US-00669753.
PR   03-MAR-1997;   97US-0039597P.
PR   03-MAR-1997;   97US-0039762P.
PR   03-MAR-1997;   97US-0039763P.
PR   02-MAR-1998;   98US-00033333.
PR   02-MAR-1998;   98US-00033428.
PR   02-MAR-1998;   98US-00033555.
PR   10-SEP-1998;   98US-00151376.
PR   02-JUN-2000; 2000US-00509591.
XX
PA   (LITT/) LITTLE A S.
PA   (LAMP/) LAMPARSKI H G.
PA   (HEND/) HENDERSON D R.
PA   (SCHU/) SCHUUR E R.
XX
PI   Little AS,  Lamparski HG,  Henderson DR,  Schuur ER;
XX
DR   WPI; 2004-119002/12.
XX
PT   Composition comprising replication competent adenovirus having adenovirus
PT   gene essential for replication under transcriptional control of cell type
PT   specific transcriptional response element and masking agent.
XX
PS   Disclosure; SEQ ID NO 7; 115pp; English.
XX
CC   This invention relates to a novel composition that contains a replication
CC   competent adenovirus capable of transfecting target host cells.
CC   Specifically, it comprises an adenoviral gene essential for replication
CC   (E1A, E1B or E4), which is under the transcriptional control of a
CC   prostate specific transcriptional response element (TRE) and polyethylene
CC   glycol (PEG) as the masking agent. The present invention describes this
CC   composition as useful for suppressing tumour cell growth and for lowering
CC   the levels of tumour cell markers. It can also be used for introducing
CC   transient expression that may be involved in treating undesired
CC   proliferations other than tumours, such as psoriatic lesions and wound
CC   healing. In addition, it is useful for detecting cells where a cell type-
CC   specific TRE is functional in a biological sample and for treating
CC   prostate-associated diseases such as hyperplasia and cancer. As such,
CC   these compositions exhibit cytostatic, antipsoriatic and vulnerary
CC   activities. This polynucleotide sequence is the human carcinoembryonic
CC   antigen (CEA) TRE DNA of the invention. NOTE: This sequence is identical
CC   to that given as SeqID 54.
XX
SQ   Sequence 472 BP; 142 A; 125 C; 134 G; 71 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 472;  DB 12;  Length 472;
  Best Local Similarity  100.0%;  Pred. No. 1.6e-126;
  Matches  472;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60

Qy         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120

Qy        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180

Qy        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240

Qy        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300

Qy        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360
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Qy        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420

Qy        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGCA 472
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGCA 472


RESULT 3
ADI36390
ID   ADI36390 standard; DNA; 472 BP.
XX
AC   ADI36390;
XX
DT   22-APR-2004  (first entry)
XX
DE   Human carcinoembryonic antigen (CEA) TRE DNA sequence SeqID 54.
XX
KW   ds; CEA; carcinoembryonic antigen; human; prostate;
KW   transcriptional response element; TRE; polyethylene glycol; PEG;
KW   masking agent; tumour cell growth; proliferation; psoriatic lesion;
KW   wound healing; hyperplasia; cancer; cytostatic; antipsoriatic; vulnerary.
XX
OS   Homo sapiens.
XX
PN   US2003152553-A1.
XX
PD   14-AUG-2003.
XX
PF   02-MAY-2002; 2002US-00139089.
XX
PR   27-JUN-1995;   95US-00495034.
PR   26-JUN-1996;   96US-00669753.
PR   03-MAR-1997;   97US-0039597P.
PR   03-MAR-1997;   97US-0039762P.
PR   03-MAR-1997;   97US-0039763P.
PR   02-MAR-1998;   98US-00033333.
PR   02-MAR-1998;   98US-00033428.
PR   02-MAR-1998;   98US-00033555.
PR   10-SEP-1998;   98US-00151376.
PR   02-JUN-2000; 2000US-00509591.
XX
PA   (LITT/) LITTLE A S.
PA   (LAMP/) LAMPARSKI H G.
PA   (HEND/) HENDERSON D R.
PA   (SCHU/) SCHUUR E R.
XX
PI   Little AS,  Lamparski HG,  Henderson DR,  Schuur ER;
XX
DR   WPI; 2004-119002/12.
XX
PT   Composition comprising replication competent adenovirus having adenovirus
PT   gene essential for replication under transcriptional control of cell type
PT   specific transcriptional response element and masking agent.
XX
PS   Example 4; SEQ ID NO 54; 115pp; English.
XX
CC   This invention relates to a novel composition that contains a replication
CC   competent adenovirus capable of transfecting target host cells.
CC   Specifically, it comprises an adenoviral gene essential for replication
CC   (E1A, E1B or E4), which is under the transcriptional control of a
CC   prostate specific transcriptional response element (TRE) and polyethylene
CC   glycol (PEG) as the masking agent. The present invention describes this
CC   composition as useful for suppressing tumour cell growth and for lowering
CC   the levels of tumour cell markers. It can also be used for introducing
CC   transient expression that may be involved in treating undesired
CC   proliferations other than tumours, such as psoriatic lesions and wound
CC   healing. In addition, it is useful for detecting cells where a cell type-
CC   specific TRE is functional in a biological sample and for treating
CC   prostate-associated diseases such as hyperplasia and cancer. As such,
CC   these compositions exhibit cytostatic, antipsoriatic and vulnerary
CC   activities. This polynucleotide sequence is a human carcinoembryonic
CC   antigen (CEA) TRE DNA sequence of the invention. NOTE: This sequence is
CC   identical to that given as SeqID 7.
XX
SQ   Sequence 472 BP; 142 A; 125 C; 134 G; 71 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 472;  DB 12;  Length 472;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-126;
  Matches  472;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60

Qy         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120

Qy        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180

Qy        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240

Qy        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300

Qy        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360

Qy        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420

Qy        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGCA 472
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGCA 472


RESULT 4
ACF62762
ID   ACF62762 standard; DNA; 3500 BP.
XX
AC   ACF62762;
XX
DT   09-OCT-2003  (first entry)
XX
DE   Human CEA genomic DNA SEQ ID NO:11.
XX
KW   Human; colon cancer; oestrogen receptor; myoglobin; p21; p27; p16; p53;
KW   progesterone receptor; pcna; CEA; cdc2; c-erbB2; methylation; CpG;
KW   characterisation; classification; diagnosis; differentiation;
KW   colon cell proliferative disorder; gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO2003014388-A2.
XX
PD   20-FEB-2003.
XX
PF   09-AUG-2002; 2002WO-EP008939.
XX
PR   09-AUG-2001; 2001DE-01039283.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Distler J,  Model F,  Taubert H;
XX
DR   WPI; 2003-256600/25.
XX
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```
PT   Determining methylation status of CpG dinucleotides using modified
PT   genomic sequences, oligonucleotides and/or PNA-oligomers, useful in the
PT   characterization, grading, staging and/or diagnosis of colon cancer.
XX
PS   Disclosure; Page 59-60; 219pp; English.
XX
CC   The present invention describes a method for determining the methylation
CC   status of CpG dinucleotides within the genes for oestrogen receptor, p21,
CC   p27, p16, progesterone receptor, myoglobin, pcna, cdc2, c-erB2, p53
CC   and/or CEA, which comprises contacting the target nucleic acid with a
CC   reagent that distinguishes between methylated and non-methylated CpG
CC   dinucleotides, and determining from the methylation status of the CpG
CC   positions the presence of a colon cancer. A set of oligomers or peptide
CC   nucleic acid (PNA)-oligomers can be used as probes for determining the
CC   cytosine methylation state and/or single nucleotide polymorphisms (SNP)
CC   of a corresponding genomic DNA by analysis of a chemically pretreated
CC   genomic DNA. The pretreated genomic DNA is useful for the determination
CC   of the methylation status of a corresponding genomic DNA and/or detection
CC   of SNPs. The methods and pretreated genomic DNA are also useful for the
CC   characterisation, classification, diagnosis and differentiation of colon
CC   cell proliferative disorders. ACF62752 to ACF63278 represent sequences
CC   used in the exemplification of the present invention
XX
SQ   Sequence 3500 BP; 843 A; 1039 C; 931 G; 687 T; 0 U; 0 Other;

  Query Match             99.8%;  Score 471;  DB 8;  Length 3500;
  Best Local Similarity   100.0%;  Pred. No. 7e-126;
  Matches  471;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2506 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 2565

Qy         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2566 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 2625

Qy        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2626 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 2685

Qy        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2686 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 2745

Qy        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2746 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 2805

Qy        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2806 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 2865

Qy        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2866 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 2925

Qy        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2926 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 2976


RESULT 5
AAQ90512
ID   AAQ90512 standard; DNA; 11288 BP.
XX
AC   AAQ90512;
XX
DT   25-MAR-2003  (revised)
DT   01-NOV-1995  (first entry)
XX
DE   CEA clone HindIII-Sau3A fragment.
XX
KW   Carcinoembryonic antigen; CEA; transcription regulatory sequence; TRS;
KW   gene targeting; cancer; metastasis; gene therapy; cytosine deaminase; ss.
XX
OS   Homo sapiens.
XX
PN   WO9514100-A2.
XX
PD   26-MAY-1995.
XX
PF   18-NOV-1994;   94WO-GB002546.
XX
PR   19-NOV-1993;   93US-00154712.
XX
PA   (WELL ) WELLCOME FOUND LTD.
XX
PI   Richards CA,  Huber B;
XX
DR   WPI; 1995-200389/26.
XX
PT   New carcinoembyronic antigen transcriptional regulatory sequence DNA -
PT   used partic. for expressing heterologous enzymes for pro-drugs in the
PT   treatment of cancers.
XX
PS   Disclosure; Page 31-37; 64pp; English.
XX
CC   CEA genomic clone lambdaCEA1 was isolated from human chromosome 19
CC   genomic library LL19NL01 (ATCC 57766). An HindIII/Sau3A fragment of the
CC   clone extended from -10.7 to +0.6 kb relative to the start site of CEA
CC   mRNA. TRS regions of CEA are used to target e.g. cytosine deaminase to
CC   cancer cells for prodrug activation. (Updated on 25-MAR-2003 to correct
CC   PN field.)
XX
SQ   Sequence 11288 BP; 2940 A; 3063 C; 2953 G; 2332 T; 0 U; 0 Other;

  Query Match             99.8%;  Score 471;  DB 2;  Length 11288;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-125;
  Matches  471;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10294 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 10353

Qy         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10354 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 10413

Qy        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10414 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 10473

Qy        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10474 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 10533

Qy        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10534 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 10593

Qy        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10594 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 10653

Qy        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10654 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 10713

Qy        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10714 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 10764


RESULT 6
AAS14778
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```
ID   AAS14778 standard; DNA; 11288 BP.
XX
AC   AAS14778;
XX
DT   27-FEB-2002  (first entry)
XX
DE   Human carcinoembryonic antigen (CEA) genomic DNA.
XX
KW   Recombinant nucleic acid vector; carcinoembryonic antigen; CEA; cytokine;
KW   syncytium-inducing polypeptide; fusogenic membrane glycoprotein; tumour;
KW   recombinase; tumour-specific promoter; hypoxic response element; HRE; ds;
KW   tyrosinase promoter; Cre; FLP; retroviral vector; malignant cell; cancer;
KW   cytostatic; gene therapy; human.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             10804. .10938
FT                   /*tag=  a
FT                   /product= "Human carcinoembryonic antigen"
XX
PN   WO200174861-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US010250.
XX
PR   31-MAR-2000; 2000US-0193977P.
XX
PA   (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
XX
PI   Vile RG,  Harrington K,  Murphy S,  Bateman A;
XX
DR   WPI; 2001-656985/75.
XX
PT   Recombinant nucleic acid vector for reducing tumor size, has expression
PT   cassette comprises a promoter linked to nucleic acid sequence encoding a
PT   syncytium-inducing polypeptide and flanked on either side by recombinase.
XX
PS   Disclosure; Fig 3; 84pp; English.
XX
CC   The invention relates to a recombinant nucleic acid vector comprising a
CC   first expression cassette, comprising a first promoter operably linked to
CC   a nucleic acid sequence encoding a syncytium-inducing polypeptide (such
CC   as a fusogenic membrane glycoprotein) and flanked on either side by a
CC   sequence recognised by a recombinase, and/or a second expression cassette
CC   comprising a tumour-specific promoter operably linked to a nucleic acid
CC   sequence encoding a recombinase. The nucleic acid of the first expression
CC   cassette may be linked to a hypoxic response element (HRE), the second
CC   expression cassette may contain a promoter linked to a nucleic acid
CC   encoding a cytokine, and a third cassette may contain a tumour specific
CC   promoter linked to the nucleic acid encoding the recombinase. The tumour
CC   specific promoter is, for example, a carcinoembryonic antigen (CEA)
CC   promoter or a tyrosinase promoter and the recombinase is, for example,
CC   Cre recombinase or FLP recombinase. The invention is useful for reducing
CC   tumour size by administering the compositions as retroviral vectors, or
CC   in a cell containing the vector, to an individual in need of treatment
CC   for a disease caused by malignant cells. This sequence represents genomic
CC   DNA encoding the human carcinoembryonic antigen (CEA)
XX
SQ   Sequence 11288 BP; 2944 A; 3060 C; 2955 G; 2329 T; 0 U; 0 Other;

  Query Match             99.8%;  Score 471;  DB 5;  Length 11288;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-125;
  Matches  471;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10294 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 10353

Qy         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10354 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 10413

Qy        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10414 TTTCTCTGTCACAAAGGAAAATAATCCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 10473

Qy        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10474 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 10533

Qy        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10534 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 10593

Qy        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10594 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 10653

Qy        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10654 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 10713

Qy        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10714 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 10764


RESULT 7
AAV52967
ID   AAV52967 standard; DNA; 15056 BP.
XX
AC   AAV52967;
XX
DT   21-DEC-1998  (first entry)
XX
DE   Carcinoembryonic antigen gene 5' flanking region.
XX
KW   Carcinoembryonic antigen; transcriptional regulatory element; CEA-TRE;
KW   human; promoter; enhancer; adenovirus; vector; cancer; gene therapy; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    14062. .14533
FT                   /*tag=  a
FT                   /label= CEA-TRE
FT                   /note= "nucleotides -402 to +69 (Claim 13)"
XX
PN   WO9839467-A2.
XX
PD   11-SEP-1998.
XX
PF   03-MAR-1998;   98WO-US004133.
XX
PR   03-MAR-1997;   97US-0039763P.
PR   02-MAR-1998;   98US-00033555.
XX
PA   (CALY-) CALYDON INC.
XX
PI   Lamparski HG,  Henerson DR,  Schuur ER;
XX
DR   WPI; 1998-495862/42.
XX
PT   New adenovirus vectors, particularly for cancer therapy - comprising
PT   adenovirus gene under transcriptional control of carcinoembryonic antigen
PT   transcriptional regulatory element.
XX
PS   Disclosure; Fig 2A-K; 95pp; English.
XX
CC   This nucleotide sequence comprises the 5' flanking region of the human
CC   carcinoembryonic antigen (CEA) gene to nucleotide +537 relative to the
CC   transcrpitional start. A 472 bp fragment (see AAV52944) of this 5'
CC   flanking region (nucleotides -402 to +69) comprises the CEA
CC   transcriptional regulatory element (CEA-TRE) that is capable of mediating
```

```
CC   gene expression specific to cells capable of expressing CEA or capable of
CC   CRE-TRE-mediated transcription. A claimed replication-competent
CC   adenovirus (Ad) vector comprises an Ad gene under transcriptional control
CC   of a CEA-TRE. By providing for transcriptional initiating regulation
CC   dependent upon CEA expression, virus replication can be restricted to
CC   target cells which allow a CEA-TRE to function, particularly carcinoma
CC   cells expressing CEA. The vectors can be used to detect and monitor
CC   samples for the presence of cells that allow a CEA-TRE to function, and
CC   to selectively kill such cells, especially malignant cells
XX
SQ   Sequence 15056 BP; 3848 A; 4125 C; 4011 G; 3072 T; 0 U; 0 Other;

  Query Match             99.8%;  Score 471;  DB 2;  Length 15056;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-125;
  Matches  471;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14062 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 14121

Qy         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14122 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 14181

Qy        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14182 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 14241

Qy        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14242 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 14301

Qy        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14302 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 14361

Qy        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14362 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 14421

Qy        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14422 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 14481

Qy        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14482 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 14532


RESULT 8
AAZ99933
ID   AAZ99933 standard; DNA; 15056 BP.
XX
AC   AAZ99933;
XX
DT   25-JUL-2000  (first entry)
XX
DE   DNA sequence of comprising a carcinoembryonic antigen TRE.
XX
KW   Carcinoembryonic antigen; adenoviral vector; adenovirus gene;
KW   transcriptional regulatory element; TRE; transcriptional control;
KW   adenoviral propagation; tumour; ss.
XX
OS   Unidentified.
XX
PN   WO200015820-A1.
XX
PD   23-MAR-2000.
XX
PF   10-SEP-1999;   99WO-US020718.
XX
PR   10-SEP-1998;   98US-0099791P.
PR   09-SEP-1999;   99US-00392822.
XX
PA   (CALY-) CALYDON INC.
XX
PI   Yu DC,  Henderson DR;
XX
DR   WPI; 2000-271456/23.
XX
PT   Adenovirus vectors comprising cell-status specific response elements
PT   useful in gene therapy protocols for the treatment of cancers.
XX
PS   Disclosure; Fig 5A-I; 79pp; English.
XX
CC   The present sequence comprises a transcriptional regulatory element (TRE)
CC   from a carcinoembryonic antigen gene. The TRE is used to produce an
CC   adenoviral vector of the invention. The specification describes an
CC   adenovirus vector which comprises an adenovirus gene under
CC   transcriptional control of a cell status specific TRE. The TRE is
CC   preferably one that is essential for adenoviral propagation. The
CC   adenovirus vectors may be used for the treatment of a range of tumours
CC   such as lung, stomach, breast, colon and rectum, and uterine and cervix
CC   cancers
XX
SQ   Sequence 15056 BP; 3848 A; 4125 C; 4011 G; 3072 T; 0 U; 0 Other;

  Query Match             99.8%;  Score 471;  DB 3;  Length 15056;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-125;
  Matches  471;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14062 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 14121

Qy         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14122 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 14181

Qy        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14182 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 14241

Qy        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14242 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 14301

Qy        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14302 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 14361

Qy        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14362 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 14421

Qy        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14422 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 14481

Qy        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14482 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 14532


RESULT 9
AAA46851
ID   AAA46851 standard; DNA; 15056 BP.
XX
AC   AAA46851;
XX
DT   03-OCT-2000  (first entry)
XX
DE   Nucleotide sequence of a CEA-TRE.
XX
KW   Adenoviral vector; adenoviral gene; E3 sequence; cancer;
KW   target cell-specific transcriptional regulatory element; TRE;
```

KW selective cytotoxicity; cell growth; tumour growth; ss.
XX
OS Homo sapiens.
XX
PN WO200039319-A2.
XX
PD 06-JUL-2000.
XX
PF 30-DEC-1999; 99WO-US031249.
XX
PR 30-DEC-1998; 98US-0114262P.
PR 29-DEC-1999; 99US-00474699.
XX
PA (CALY-) CALYDON INC.
XX
PI Henderson DR, Yu D;
XX
DR WPI; 2000-452409/39.
XX
PT New adenoviral vector for selective targeting of cancer cells, comprises
PT an adenovirus gene under transcriptional control of a target cell-
PT specific transcriptional regulatory element and an E3 sequence.
XX
PS Disclosure; Fig 23; 138pp; English.
XX
CC The specification describes an adenoviral vector which comprises an
CC adenoviral gene under the transcriptional control of a target cell-
CC specific transcriptional regulatory element (TRE) and an E3 sequence. The
CC vectors are useful for exerting selective cytotoxicity and/or suppressing
CC cell growth (including tumour growth). This is especially useful in
CC treating cancer in which targeted cell killing is desirable. This is also
CC useful for targeted cytotoxic effects in other, non-tumour cells, when
CC selective destruction and/or suppression of these cells is desirable. The
CC vectors can also be useful for detecting the presence of cells which
CC permit function of a target cell-specific TRE in, for example, an
CC appropriate biological (such as clinical) sample. The adenovirus
CC vector(s) can optionally selectively produce one or more proteins of
CC interest in a target cell by using a heterologous, i.e., non-adenoviral,
CC TRE. The present sequence represents a CEA-TRE, which is used in the
CC course of the invention
XX
SQ Sequence 15056 BP; 3848 A; 4125 C; 4011 G; 3072 T; 0 U; 0 Other;

Query Match 99.8%; Score 471; DB 3; Length 15056;
Best Local Similarity 100.0%; Pred. No. 1.3e-125;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14062 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 14121

Qy         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14122 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 14181

Qy        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14182 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 14241

Qy        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14242 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 14301

Qy        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14302 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 14361

Qy        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14362 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 14421

Qy        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14422 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 14481

Qy        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14482 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 14532
```

RESULT 10
AAH43620
ID AAH43620 standard; cDNA; 15056 BP.
XX
AC AAH43620;
XX
DT 07-JAN-2002 (first entry)
XX
DE CEA-TRE.
XX
KW Adenovirus; ADP; replication-competent; adenoviral vector; TRE; PCR;
KW transcriptional regulatory element; mutation; deletion; IRES; primer;
KW promoter; internal ribosome entry site; cytotoxic; cancer; bladder;
KW amplify; polymerase chain reaction; alpha-fetoprotein; AFP; EMCV;
KW encephalomycarditis virus; vascular endothelial growth factor; VEGF;
KW immunoglobulin heavy-chain binding protein; BiP; uroplakin II; PDGF;
KW platelet derived growth factor; hypoxia responsive element; HRE;
KW prostate-specific antigen; PSA; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT precursor_RNA 14466. .15056
FT /*tag= a
FT /note= "Transcription start site"
XX
PN WO200173093-A2.
XX
PD 04-OCT-2001.
XX
PF 21-MAR-2001; 2001WO-US009036.
XX
PR 24-MAR-2000; 2000US-0192156P.
XX
PA (CALY-) CALYDON INC.
XX
PI Yu D, Li Y, Henderson DR;
XX
DR WPI; 2001-639234/73.
XX
PT Replication-competent adenoviral vector, useful e.g. for killing cancer
PT cells, contains two genes linked by internal ribosome entry site and
PT controlled by target-specific regulator.
XX
PS Example; Page 117-125; 148pp; English.
XX
CC The sequences given in AAH43607-22 represent sequences which may used in
CC the replication-competent adenoviral vector (A) of the invention. The
CC vector contains two genes (G1, G2) that are co-transcribed as a single
CC mRNA and under control of a heterologous, target cell-specific
CC transcriptional regulatory element (TRE). G2 has a mutation in, or
CC deletion of, its endogenous promoter and is controlled from an internal
CC ribosome entry site (IRES). (A) has greater specificity for a target cell
CC than a similar vector in which TRE is operably linked to a gene and which
CC lacks an IRES. (A) are used to modify the genotype of target cells,
CC optionally in vitro with subsequent return of altered cells to the host
CC and where G2 is a cytotoxic gene, to confer selective cyto- toxicity to
CC target cells, especially for killing cancer cells. Also (A) are used for
CC diagnosis and monitoring, e.g. detection of bladder cancer cells. The
CC target cell-specific TRE ensures that (A) has better targeting
CC specificity, with minimal replication in non-target cells, so a runaway
CC infection is prevented but production of adenoviral proteins in target
CC cells activates and/or stimulates the immune response against target
CC cells producing such proteins. The use of an IRES (rather than two
CC identical control elements) eliminates the risk of homologous
CC recombination and may provide enough extra space for an additional

```
CC   (therapeutic) gene
XX
SQ   Sequence 15056 BP; 3848 A; 4125 C; 4011 G; 3072 T; 0 U; 0 Other;

  Query Match            99.8%;  Score 471;  DB 5;  Length 15056;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-125;
  Matches  471;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14062 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 14121

Qy         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14122 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 14181

Qy        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14182 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 14241

Qy        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14242 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 14301

Qy        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14302 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 14361

Qy        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14362 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 14421

Qy        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14422 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 14481

Qy        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14482 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 14532


RESULT 11
AAF87238
ID   AAF87238 standard; DNA; 15056 BP.
XX
AC   AAF87238;
XX
DT   26-MAR-2002  (first entry)
XX
DE   CEA-TRE fusion protein coding sequence.
XX
KW   Tumour growth suppression; adenovirus vector; antineoplastic agent;
KW   transcriptional regulatory element; TRE; radiotherapy; bladder cancer;
KW   prostate cancer; liver cancer; breast cancer; colon cancer; melanoma;
KW   ovarian cancer; pancreatic cancer; lung cancer; brain cancer; therapy;
KW   CEA-TRE; ds.
XX
OS   Homo sapiens.
XX
PN   WO200172341-A2.
XX
PD   04-OCT-2001.
XX
PF   21-MAR-2001; 2001WO-US009042.
XX
PR   24-MAR-2000; 2000US-0192015P.
XX
PA   (CALY-) CALYDON INC.
XX
PI   Yu D,  Chen Y,  Henderson DR;
XX
DR   WPI; 2001-648426/74.
XX
PT   Suppression of tumor growth, e.g. liver, bladder or breast cancer,
PT   comprises using a synergistic combination of adenovirus vector and
PT   antineoplastic agent or radiotherapy.
XX
PS   Claim 12; Page 185-193; 248pp; English.
XX
CC   This sequence represents a CEA-TRE fusion protein coding sequence used in
CC   the scope of the invention. The invention relates to a method for the
CC   suppression of tumour growth comprising the administration of: (a) a
CC   target cell-specific adenovirus vector comprising an adenoviral gene
CC   essential for replication under transcriptional control of a target cell-
CC   specific transcriptional regulatory element (TRE); and (b) at least one
CC   antineoplastic agent; or (c) a course of radiotherapy where the amount of
CC   (a) and/or (b) or (c) is lower than that known to be effective for
CC   suppressing tumour growth when administered alone. The method is used for
CC   suppression of tumour growth for treatment of e.g. bladder cancer,
CC   prostate cancer, liver cancer, breast cancer, colon cancer, melanoma,
CC   ovarian cancer, pancreatic cancer, lung cancer or brain cancer. The
CC   combinations enhance the efficacy of treatment, allowing lower doses to
CC   be administered, reducing toxicity and suffering of the patient
XX
SQ   Sequence 15056 BP; 3848 A; 4126 C; 4010 G; 3072 T; 0 U; 0 Other;

  Query Match            99.8%;  Score 471;  DB 5;  Length 15056;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-125;
  Matches  471;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14062 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 14121

Qy         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14122 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 14181

Qy        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14182 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 14241

Qy        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14242 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 14301

Qy        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14302 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 14361

Qy        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14362 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 14421

Qy        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14422 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 14481

Qy        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14482 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 14532


RESULT 12
ABK99582
ID   ABK99582 standard; DNA; 15056 BP.
XX
AC   ABK99582;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Prostate-specific antigen transcriptional regulatory elelment (TRE).
XX
KW   Adenovirus; transcriptional regulatory element; TRE; prostate; liver;
KW   breast cancer; colon cancer; antitumour; gene; ds; probasin; PB; human;
KW   rat; carcinoembryonic antigen; prostate-specific antigen; ADP;
```

```
KW   adenovirus death protein; glandular kallikrein.
XX
OS   Unidentified.
XX
PN   US2002068049-A1.
XX
PD   06-JUN-2002.
XX
PF   06-DEC-2000; 2000US-00732169.
XX
PR   10-SEP-1998;   98US-00151376.
XX
PA   (HEND/) HENDERSON D R.
PA   (SCHU/) SCHUUR E R.
XX
PI   Henderson DR,  Schuur ER;
XX
DR   WPI; 2002-582468/62.
XX
PT   Novel adenovirus vector comprises adenovirus gene under transcriptional
PT   control of cell-type specific transcriptional response element for
PT   conferring selective toxicity on target cell and for suppressing tumor
PT   growth.
XX
PS   Disclosure; Fig 15; 83pp; English.
XX
CC   The invention relates to an adenovirus vector (AV) comprising an AV gene
CC   under transcriptional control of a cell type-specific transcriptional
CC   regulatory element (TRE) and optionally a first AV gene under control of
CC   a first cell type-specific TRE and a second gene under control of a
CC   second cell type-specific TRE, where the first and second cell type-
CC   specific TREs are substantially identical. When the vector is introduced
CC   into a cell (e.g. prostate cell, liver cell, breast cancer cell or colon
CC   cancer cell) it allows the cell type-specific TRE to function, resulting
CC   in cytotoxicity. The vector is useful for suppressing tumour growth of a
CC   target cell. This sequence represents a polynucleotide used in the scope
CC   of the invention
XX
SQ   Sequence 15056 BP; 3848 A; 4125 C; 4011 G; 3072 T; 0 U; 0 Other;

  Query Match             99.8%;  Score 471;  DB 6;  Length 15056;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-125;
  Matches  471;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14062 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 14121

Qy         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14122 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 14181

Qy        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14182 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 14241

Qy        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14242 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 14301

Qy        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14302 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 14361

Qy        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14362 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 14421

Qy        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14422 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 14481

Qy        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14482 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 14532


RESULT 13
ACD07309
ID   ACD07309 standard; DNA; 15056 BP.
XX
AC   ACD07309;
XX
DT   07-AUG-2003  (first entry)
XX
DE   Human carcinoembryonic antigen (CEA) TRE.
XX
KW   Adenoviral vector; adenovirus gene; transcriptional control; TRE;
KW   cell type-specific; transcriptional response element; PSA; hKLK;
KW   prostate-specific antigen; glandular kallikrein; probastin; PB;
KW   carcinoembryonic antigen; CEA; mucin-like glycoprotein DF3; MUC1;
KW   cytotoxicity; neoplasia; tumour growth; gene therapy; cytostatic; human;
KW   ds.
XX
OS   Homo sapiens.
XX
PN   US2003044383-A1.
XX
PD   06-MAR-2003.
XX
PF   10-SEP-1998;   98US-00151376.
XX
PR   27-JUN-1995;   95US-00495034.
PR   20-AUG-1996;   96US-00699753.
PR   03-MAR-1997;   97US-0039597P.
PR   03-MAR-1997;   97US-0039599P.
PR   03-MAR-1997;   97US-0039762P.
PR   03-MAR-1997;   97US-0039763P.
PR   02-MAR-1998;   98US-00033333.
PR   02-MAR-1998;   98US-00033428.
PR   02-MAR-1998;   98US-00033555.
XX
PA   (HEND/) HENDERSON D R.
PA   (SCHU/) SCHUUR E R.
XX
PI   Henderson DR,  Schuur ER;
XX
DR   WPI; 2003-456547/43.
XX
PT   New adenovirus vector for transfecting target host cells, comprises an
PT   adenovirus gene under transcriptional control of a cell type-specific
PT   transcriptional response element.
XX
PS   Disclosure; Fig 14; 83pp; English.
XX
CC   The present invention relates to adenoviral vectors comprising an
CC   adenovirus gene under transcriptional control of a cell type-specific
CC   transcriptional response element (TRE). Example TREs given in the
CC   specification include human prostate-specific antigen (PSA) TRE, human
CC   glandular kallikrein (hKLK) TRE, rat probastin (PB) TRE, human
CC   carcinoembryonic antigen (CEA) TRE, and human mucin-like glycoprotein DF3
CC   (MUC1) TRE. The modified adenovirus vector is useful as a vehicle for
CC   introducing new genetic capability, particularly associated with
CC   cytotoxicity for treating neoplasia. For example, the vector may be used
CC   in a target cell to suppress tumour growth, or to kill the target cell.
CC   The vector is particularly useful in gene therapy. The present sequence
CC   represents a TRE
XX
SQ   Sequence 15056 BP; 3848 A; 4125 C; 4011 G; 3072 T; 0 U; 0 Other;

  Query Match             99.8%;  Score 471;  DB 8;  Length 15056;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-125;
  Matches  471;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db      14062 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 14121

Qy         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14122 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 14181

Qy        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14182 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 14241

Qy        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14242 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 14301

Qy        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14302 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 14361

Qy        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14362 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 14421

Qy        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14422 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 14481

Qy        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14482 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 14532
```

RESULT 14
ADB54000
ID ADB54000 standard; DNA; 4138 BP.
XX
AC ADB54000;
XX
DT 04-DEC-2003 (first entry)
XX
DE CEA genomic DNA region.
XX
KW colon cell proliferative disorder; non methylated CpG dinucleotide;
KW cytostatic; cancer; adenoma; carcinoma; cytosine methylation state; ds.
XX
OS Unidentified.
XX
PN WO2003072821-A2.
XX
PD 04-SEP-2003.
XX
PF 27-FEB-2003; 2003WO-EP002035.
XX
PR 27-FEB-2002; 2002EP-00004551.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Adorjan P, Burger M, Maier S, Nimmrich I, Becker E, Lesche R;
PI Rujan T, Schmitt A;
XX
DR WPI; 2003-731620/69.
XX
PT Detecting and differentiating between colon cell proliferative disorders
PT associated with a gene or its regulatory regions comprises contacting a
PT target nucleic acid in a biological sample obtained from the subject with
PT a reagent.
XX
PS Claim 46; SEQ ID NO 56; 74pp; English.
XX
CC The invention relates to a novel method for detecting and differentiating
CC between colon cell proliferative disorders associated with at least one
CC gene or its regulatory regions. The method comprises contacting a target
CC nucleic acid in a biological sample obtained from the subject with at
CC least one reagent or a series of reagents, where the reagent or series of
CC reagents, distinguishes between methylated and non methylated CpG
CC dinucleotides within the target nucleic acid. The molecules of the
CC invention demonstrate cytostatic activity whilst the method may useful
CC for detecting and differentiating between colon cell proliferative
CC disorders, including cancers such as colon adenoma and colon carcinoma.
CC The PNA (peptide nucleic acid)-oligomers are useful as probes for
CC determining cytosine methylation state or single nucleotide
CC polymorphisms. The current sequence is that of the genomic DNA region of
CC the invention. This sequence is not shown within the specification but is
CC taken from Wipoweb.
XX
SQ Sequence 4138 BP; 1048 A; 1201 C; 1059 G; 830 T; 0 U; 0 Other;

  Query Match   96.6%; Score 455.8; DB 10; Length 4138;
  Best Local Similarity 99.4%; Pred. No. 1.9e-121;
  Matches 468; Conservative   0; Mismatches   2; Indels   1; Gaps   1;

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Qy          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2109 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 2168

Qy         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2169 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 2228

Qy        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2229 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 2288

Qy        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||  ||||||||
Db       2289 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTGGATCCACCTT 2348

Qy        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300
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Db       2349 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 2408

Qy        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db       2409 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCC-TGACCCA 2467

Qy        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2468 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 2527

Qy        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2528 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 2578
```

RESULT 15
ADC37109
ID ADC37109 standard; DNA; 3281 BP.
XX
AC ADC37109;
XX
DT 18-DEC-2003 (first entry)
XX
DE DNA of a human carcinoembryonic antigen, CEA, gene.
XX
KW DNA vaccine; immune response; carcinoembryonic antigen; CEA; CD40 ligand;
KW homotrimer; cytostatic; gene therapy; cancer; colon cancer; human; gene;
KW ds.
XX
OS Homo sapiens.
XX
PN WO2003074712-A1.
XX
PD 12-SEP-2003.
XX
PF 28-FEB-2003; 2003WO-US006295.
XX
PR 02-MAR-2002; 2002US-00090238.

XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Xiang R, Reisfeld RA;
XX
DR WPI; 2003-748281/70.
XX
PT New DNA vaccine for eliciting an immune response against cells presenting
PT a carcinoembryonic antigen (CEA) such as colon cancer cells, comprises
PT plasmid DNAs encoding a CEA and/or a CD40 ligand, together with a
PT carrier.
XX
PS Disclosure; SEQ ID NO 1; 48pp; English.
XX
CC The invention relates to a novel DNA vaccine for eliciting an immune
CC response against cells that present a carcinoembryonic antigen (CEA). The
CC vaccine comprises a plasmid DNA operably encoding a CEA, and a plasmid
CC DNA operably encoding a CD40 ligand or its homotrimer, together with a
CC carrier. The DNA vaccine has cytostatic activity and may be used in gene
CC therapy to treat disorders. The DNA vaccine is useful in preventing
CC cancers, such as colon cancer, by eliciting an immune response against
CC cells that present CEA, including colon cancer cells. This polynucleotide
CC sequence represents the DNA of a human CEA gene, used as a ligand of the
CC invention.
XX
SQ Sequence 3281 BP; 847 A; 953 C; 871 G; 610 T; 0 U; 0 Other;

Query Match 91.6%; Score 432.4; DB 10; Length 3281;
Best Local Similarity 98.9%; Pred. No. 1.1e-114;
Matches 467; Conservative 0; Mismatches 1; Indels 4; Gaps 3;

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Qy          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 1320

Qy         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db       1321 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGA-CCTGCTGGG 1379

Qy        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1380 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 1439

Qy        181 CAGAGGTCAGCACTGGGG-AAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCT 239
              |||||||||||||||||  |||||||||||||  | ||||||||||||||||||||||||
Db       1440 CAGAGGTCAGCACTGGGGAAAGACAGGTTGTC--CACAGGGGATGGGGGTCCATCCACCT 1497

Qy        240 TGCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAG 299
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1498 TGCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAG 1557

Qy        300 AGGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCC 359
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1558 AGGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCC 1617

Qy        360 ACGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGAC 419
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1618 ACGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGAC 1677

Qy        420 AGCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1678 AGCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 1729
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Search completed: December 11, 2004, 06:59:41
Job time : 430 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 11, 2004, 06:33:08 ; Search time 90 Seconds
(without alignments)
3727.693 Million cell updates/sec

Title: US-10-045-116-1
Perfect score: 472
Sequence: 1 AGCCACCACCCAGTGAGCCT.....ACGTTCCTGGAACTCAAGCA 472

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	2	472	100.0	472	4	US-09-151-376-7	Sequence 7, Appli
	3	472	100.0	472	4	US-09-151-376-54	Sequence 54, Appl
	4	471	99.8	11288	3	US-08-646-301A-1	Sequence 1, Appli
	5	471	99.8	11288	3	US-08-481-968A-4	Sequence 4, Appli
	6	471	99.8	11288	3	US-08-154-712B-4	Sequence 4, Appli
	7	471	99.8	11288	4	US-09-947-925A-4	Sequence 4, Appli
	8	471	99.8	15056	4	US-09-474-699-10	Sequence 10, Appl
	9	471	99.8	15056	4	US-09-814-351-14	Sequence 14, Appl
	10	156.6	33.2	2073	4	US-09-924-103-1	Sequence 1, Appli
	11	94	19.9	3774	3	US-08-646-301A-2	Sequence 2, Appli
	12	94	19.9	3774	3	US-08-481-968A-5	Sequence 5, Appli
	13	94	19.9	3774	3	US-08-154-712B-5	Sequence 5, Appli
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c	15	71.2	15.1	7218	1	US-08-232-463-14	Sequence 14, Appl
	16	57.6	12.2	387	4	US-09-370-838-177	Sequence 177, App
	17	57.6	12.2	387	4	US-09-854-133-177	Sequence 177, App
	18	57.2	12.1	460	4	US-09-401-064-169	Sequence 169, App
	19	56.4	11.9	319	4	US-09-513-999C-14905	Sequence 14905, A
	20	54.8	11.6	306	4	US-09-513-999C-14903	Sequence 14903, A
	21	54.8	11.6	327	4	US-09-513-999C-14902	Sequence 14902, A
	22	54.8	11.6	414	4	US-09-513-999C-14904	Sequence 14904, A
	23	54.6	11.6	504	4	US-09-513-999C-14906	Sequence 14906, A
	24	54.2	11.5	502	4	US-09-513-999C-8661	Sequence 8661, Ap
	25	54.2	11.5	2115	4	US-09-513-999C-14901	Sequence 14901, A
	26	54	11.4	2220	1	US-08-389-459A-16	Sequence 16, Appl
	27	54	11.4	2220	3	US-08-987-867A-16	Sequence 16, Appl
	28	53.4	11.3	525	4	US-09-513-999C-3741	Sequence 3741, Ap
c	29	44.2	9.4	319	3	US-09-385-982-486	Sequence 486, App
c	30	40.4	8.6	505	4	US-09-621-976-15639	Sequence 15639, A
	31	39.2	8.3	289	3	US-09-007-005-17	Sequence 17, Appl
	32	39.2	8.3	289	3	US-09-244-796-17	Sequence 17, Appl
	33	38	8.1	7898	3	US-08-984-709A-49	Sequence 49, Appl
	34	37.6	8.0	439	4	US-09-513-999C-14899	Sequence 14899, A
	35	37	7.8	1413	3	US-08-984-709A-52	Sequence 52, Appl
	36	36.2	7.7	432	4	US-09-513-999C-8272	Sequence 8272, Ap
	37	35.6	7.5	50	1	US-08-171-389-392	Sequence 392, App
	38	35.6	7.5	50	1	US-08-123-936-392	Sequence 392, App
	39	35.6	7.5	50	2	US-08-475-228A-392	Sequence 392, App
	40	35.6	7.5	50	3	US-08-482-080A-392	Sequence 392, App
	41	35.6	7.5	50	3	US-09-354-947-392	Sequence 392, App
	42	35.6	7.5	50	5	PCT-US93-12388-392	Sequence 392, App
c	43	35.6	7.5	545	4	US-09-270-767-2655	Sequence 2655, Ap
c	44	35.6	7.5	545	4	US-09-270-767-17937	Sequence 17937, A
c	45	34.2	7.2	335	4	US-09-621-976-13385	Sequence 13385, A

ALIGNMENTS

RESULT 1
US-09-033-556-7
; Sequence 7, Application US/09033556
; Patent No. 6432700
; GENERAL INFORMATION:
; APPLICANT: Henderson, Daniel R.
; APPLICANT: Yu, De Chao
; TITLE OF INVENTION: ADENOVIRUS VECTORS CONTAINING
; TITLE OF INVENTION: HETEROLOGOUS TRANSCRIPTION REGULATORY ELEMENTS AND METHODS
; TITLE OF INVENTION: OF USING SAME
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/033,556
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Catherine, Polizzi M
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 34802-20010.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 472 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-033-556-7

Query Match 100.0%; Score 472; DB 4; Length 472;
Best Local Similarity 100.0%; Pred. No. 9.2e-134;
Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60

Qy         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180

Qy        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240

Qy        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300

Qy        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360

Qy        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420

Qy        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGCA 472
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGCA 472
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RESULT 2
US-09-151-376-7
; Sequence 7, Application US/09151376
; Patent No. 6676935
; GENERAL INFORMATION:
; APPLICANT: Henderson, D.R.
; APPLICANT: Schuur, E.R.
; TITLE OF INVENTION: TISSUE SPECIFIC VIRAL VECTORS
; FILE REFERENCE: 348022000221
; CURRENT APPLICATION NUMBER: US/09/151,376
; CURRENT FILING DATE: 1998-09-10
; EARLIER APPLICATION NUMBER: 08/669,753
; EARLIER FILING DATE: 1996-06-26
; EARLIER APPLICATION NUMBER: 08/495,034
; EARLIER FILING DATE: 1995-06-27
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 472
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-151-376-7

Query Match 100.0%; Score 472; DB 4; Length 472;
Best Local Similarity 100.0%; Pred. No. 9.2e-134;
Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60

Qy         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120

Qy        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180

Qy        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240

Qy        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300

Qy        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360

Qy        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420

Qy        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGCA 472
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGCA 472
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RESULT 3
US-09-151-376-54
; Sequence 54, Application US/09151376
; Patent No. 6676935
; GENERAL INFORMATION:
; APPLICANT: Henderson, D.R.
; APPLICANT: Schuur, E.R.
; TITLE OF INVENTION: TISSUE SPECIFIC VIRAL VECTORS
; FILE REFERENCE: 348022000221
; CURRENT APPLICATION NUMBER: US/09/151,376
; CURRENT FILING DATE: 1998-09-10
; EARLIER APPLICATION NUMBER: 08/669,753
; EARLIER FILING DATE: 1996-06-26
; EARLIER APPLICATION NUMBER: 08/495,034
; EARLIER FILING DATE: 1995-06-27
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 54
; LENGTH: 472
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Unknown
US-09-151-376-54

Query Match 100.0%; Score 472; DB 4; Length 472;
Best Local Similarity 100.0%; Pred. No. 9.2e-134;
Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60

Qy         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120

Qy        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180

Qy        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240

Qy        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300

Qy        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360
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Qy        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420

Qy        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGCA 472
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGCA 472


RESULT 4
US-08-646-301A-1
; Sequence 1, Application US/08646301A
; Patent No. 6194211
; GENERAL INFORMATION:
;  APPLICANT:  Richards, Cynthia Ann
;  APPLICANT:  Huber, Brian E.
;  TITLE OF INVENTION:  Transcriptional Regulatory Sequence of Carcinoembryonic
; Patent No. 6194211
;  TITLE OF INVENTION:  Antigen for Expression Targeting
;  FILE REFERENCE:  PB1508USW
;  CURRENT APPLICATION NUMBER: US/08/646,301A
;  CURRENT FILING DATE:  1996-05-16
;  NUMBER OF SEQ ID NOS:  25
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 11288
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-08-646-301A-1

  Query Match             99.8%;  Score 471;  DB 3;  Length 11288;
  Best Local Similarity   100.0%;  Pred. No. 8.4e-133;
  Matches  471;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10294 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 10353

Qy         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10354 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 10413

Qy        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10414 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 10473

Qy        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10474 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 10533

Qy        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10534 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 10593

Qy        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10594 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 10653

Qy        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10654 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 10713

Qy        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10714 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 10764


RESULT 5
US-08-481-968A-4
; Sequence 4, Application US/08481968A
; Patent No. 6300490
; GENERAL INFORMATION:
;  APPLICANT:  Huber, Brian
;  APPLICANT:  Richards, Cynthia
;  TITLE OF INVENTION:  Molecular Constructs Comprising a Carcinoembryonic Antigen (CEA
;  TITLE OF INVENTION:  Transcriptional Regulatory Region
;  FILE REFERENCE:  PB1087US4
;  CURRENT APPLICATION NUMBER: US/08/481,968A
;  CURRENT FILING DATE:  1998-06-07
;  NUMBER OF SEQ ID NOS:  36
;  SOFTWARE:  PatentIn version 3.0
; SEQ ID NO 4
;   LENGTH: 11288
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-08-481-968A-4

  Query Match             99.8%;  Score 471;  DB 3;  Length 11288;
  Best Local Similarity   100.0%;  Pred. No. 8.4e-133;
  Matches  471;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10294 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 10353

Qy         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10354 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 10413

Qy        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10414 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 10473

Qy        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10474 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 10533

Qy        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10534 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 10593

Qy        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10594 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 10653

Qy        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10654 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 10713

Qy        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10714 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 10764


RESULT 6
US-08-154-712B-4
; Sequence 4, Application US/08154712B
; Patent No. 6337209
; GENERAL INFORMATION:
;  APPLICANT:  Huber, Brian
;  APPLICANT:  Richards, Cynthia
;  TITLE OF INVENTION:  Molecular Constructs Containing a Carcinoembryonic Antigen Regu
;  TITLE OF INVENTION:  Sequence
;  FILE REFERENCE:  PB1087US3
;  CURRENT APPLICATION NUMBER: US/08/154,712B
;  CURRENT FILING DATE:  1993-11-19
;  NUMBER OF SEQ ID NOS:  36
;  SOFTWARE:  PatentIn version 3.0
; SEQ ID NO 4
;   LENGTH: 11288
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-08-154-712B-4

  Query Match             99.8%;  Score 471;  DB 3;  Length 11288;
  Best Local Similarity   100.0%;  Pred. No. 8.4e-133;
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  Matches  471;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10294 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 10353

Qy         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10354 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 10413

Qy        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10414 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 10473

Qy        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10474 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 10533

Qy        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10534 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 10593

Qy        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10594 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 10653

Qy        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10654 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 10713

Qy        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10714 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 10764


RESULT 7
US-09-947-925A-4
; Sequence 4, Application US/09947925A
; Patent No. 6699690
; GENERAL INFORMATION:
;  APPLICANT: Huber, Brian
;  APPLICANT:  Richards, Cynthia
;  TITLE OF INVENTION: Molecular Constructs Containing a Carcinoembryonic
;  TITLE OF INVENTION:  Antigen Regulatory
;  TITLE OF INVENTION:  Sequence
;  FILE REFERENCE: PB1087US3
;  CURRENT APPLICATION NUMBER: US/09/947,925A
;  CURRENT FILING DATE:  2001-09-06
;  PRIOR APPLICATION NUMBER: US/08/154,712
;  PRIOR FILING DATE: 1993-11-19
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
;   LENGTH: 11288
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-947-925A-4

  Query Match             99.8%;  Score 471;  DB 4;  Length 11288;
  Best Local Similarity   100.0%;  Pred. No. 8.4e-133;
  Matches  471;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10294 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 10353

Qy         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10354 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 10413

Qy        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10414 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 10473

Qy        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10474 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 10533

Qy        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10534 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 10593

Qy        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10594 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 10653

Qy        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10654 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 10713

Qy        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10714 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 10764


RESULT 8
US-09-474-699-10
; Sequence 10, Application US/09474699
; Patent No. 6495130
; GENERAL INFORMATION:
;  APPLICANT:  Henderson, Daniel R.
;  APPLICANT:  Yu, De Chao
;  TITLE OF INVENTION:  TARGET CELL-SPECIFIC ADENOVIRAL VECTORS
;  TITLE OF INVENTION:  CONTAINING E3 AND METHODS OF USE THEREOF
;  FILE REFERENCE:  348022001300
;  CURRENT APPLICATION NUMBER: US/09/474,699
;  CURRENT FILING DATE:  1999-12-29
;  PRIOR APPLICATION NUMBER:  60/114,262
;  PRIOR FILING DATE:  1998-12-30
;  NUMBER OF SEQ ID NOS:  23
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 10
;   LENGTH: 15056
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-09-474-699-10

  Query Match             99.8%;  Score 471;  DB 4;  Length 15056;
  Best Local Similarity   100.0%;  Pred. No. 9.6e-133;
  Matches  471;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14062 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 14121

Qy         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14122 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 14181

Qy        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14182 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 14241

Qy        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14242 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 14301

Qy        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14302 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 14361

Qy        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14362 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 14421

Qy        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14422 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 14481

Qy        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 471
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14482 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 14532


RESULT 9
US-09-814-351-14
; Sequence 14, Application US/09814351
; Patent No. 6692736
; GENERAL INFORMATION:
;  APPLICANT: Yu, De-Chao
;  APPLICANT:  Li, Yuanhao
;  APPLICANT:  Henderson, Daniel R.
;  TITLE OF INVENTION: CELL-SPECIFIC ADENOVIRUS VECTORS
;  TITLE OF INVENTION:  COMPRISING AN INTERNAL RIBOSOME ENTRY SITE
;  FILE REFERENCE: 348022001700
;  CURRENT APPLICATION NUMBER: US/09/814,351
;  CURRENT FILING DATE:  2001-03-21
;  PRIOR APPLICATION NUMBER: 60/192,156
;  PRIOR FILING DATE: 2000-03-24
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
;   LENGTH: 15056
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: CEA TRE
US-09-814-351-14

  Query Match             99.8%;  Score 471;  DB 4;  Length 15056;
  Best Local Similarity   100.0%;  Pred. No. 9.6e-133;
  Matches  471;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14062 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 14121

Qy         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14122 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 14181

Qy        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14182 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 14241

Qy        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14242 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 14301

Qy        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14302 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 14361

Qy        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14362 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 14421

Qy        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14422 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 14481

Qy        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 471
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14482 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 14532


RESULT 10
US-09-924-103-1
; Sequence 1, Application US/09924103
; Patent No. 6759045
; GENERAL INFORMATION:
;  APPLICANT: GOLDENBERG, DAVID M.
;  APPLICANT:  HANSEN, HANS J.
;  TITLE OF INVENTION: IMMUNOTHERAPY FOR CHRONIC MYELOCYTIC LEUKEMIA
;  FILE REFERENCE: 018733-1055
;  CURRENT APPLICATION NUMBER: US/09/924,103
;  CURRENT FILING DATE:  2001-08-08
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 2073
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-924-103-1

  Query Match             33.2%;  Score 156.6;  DB 4;  Length 2073;
  Best Local Similarity   76.0%;  Pred. No. 1.2e-37;
  Matches  247;  Conservative    0;  Mismatches   69;  Indels    9;  Gaps    4;

Qy        156 TGACAGACCCAAGGACAGAACACAGCAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCC 215
                |||||||||||||| |   |||||||||||||| |  |||||||   | ||| |||||
Db        220 TGACAGACCCAAGGCCCAGACACAGCAGAGGTCCGTGCTGGGGAGAGCGGGTCGTCCTGT 279

Qy        216 CAGGGGATGGGGGTCCATCCACCTT---GCCGAAAAGATTTGTCTGAGGAACTGA----A 268
                | || |  ||||||||  ||   |     | | ||  |  |||| ||||||||    |
Db        280 TATGGAACAGGGGTCCAAACAAGCTTGCTTCTCAGAGCATCTTCTGGGGAACTGAATATA 339

Qy        269 AATAGAAGGGAAAAAAGAGGAGGGACAAAAGAGGCAGAAATGAGAGGGGAGGGGACAGAG 328
                || |||| || || | ||||||||||||||||| ||||||||||||||||||||| ||||
Db        340 AACAGAAAGGGAAGAGGAGGAGGGACAAAAGAGACAGAAATGAGAGGGGAGGGGATAGAG 399

Qy        329 GACACCTGAATAAAGACCACACCCATGACCCACGTGATGCTGAGAAGTACTCCT-GCCCT 387
                ||  |||||| | ||||| |||||||||||||||||  ||| ||| | || ||  ||||
Db        400 GATTCCTGAACAGAGACCGCACCCATGACCCACGTGACCCTGGGAAATGCTTCTATCCCT 459

Qy        388 AGGAAGAGACTCAGGGCAGAGGGAGGAAGGACAGCAGACCAGACAGTCACAGCAGCCTTG 447
                || ||| |||||  |||| |||||||||||||||  |  |||||||||||||| ||
Db        460 GAGAGGAGGCTCAGCACAGAAGGAGGAAGGACAGCAGGGCCAACAGTCACAGCAGCCCTG 519

Qy        448 A-CAAAACGTTCCTGGAACTCAAGC 471
                | || | | |||||||| |||||||
Db        520 ACCAGAGCATTCCTGGAGCTCAAGC 544


RESULT 11
US-08-646-301A-2
; Sequence 2, Application US/08646301A
; Patent No. 6194211
; GENERAL INFORMATION:
;  APPLICANT:  Richards, Cynthia Ann
;  APPLICANT:  Huber, Brian E.
;  TITLE OF INVENTION:  Transcriptional Regulatory Sequence of Carcinoembryonic
; Patent No. 6194211
;  TITLE OF INVENTION:  Antigen for Expression Targeting
;  FILE REFERENCE:  PB1508USW
;  CURRENT APPLICATION NUMBER: US/08/646,301A
;  CURRENT FILING DATE:  1996-05-16
;  NUMBER OF SEQ ID NOS:  25
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 3774
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-08-646-301A-2

  Query Match             19.9%;  Score 94;  DB 3;  Length 3774;
  Best Local Similarity   69.5%;  Pred. No. 1.7e-18;
  Matches  185;  Conservative    0;  Mismatches   50;  Indels   31;  Gaps    3;

Qy          4 CACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTGGGC 63
                ||  |  ||||||||  | || ||||||||||||||||||||||||||||||| |||||
Db       1662 CAGTAAACAGTGAGCTCCTATCCAGCCCCCAGAGCCACCTCTGTCACCTTCCTGCTGGGC 1721
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Qy         64 ATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGGTTT 123
              ||||||||||||||| || ||| ||  |||||||||||||||| ||   |  ||||||||
Db       1722 ATCATCCCACCTTCACA-AGCACTAAAGAGCATGGGGAGACCTGG---CTAGCTGGGTTT 1777

Qy        124 CTCTGTCACAAAGGAAAATAATCCCCCTGGT--------------------------GT 156
              ||   |||||||| |||  |  ||||  | |                          |
Db       1778 CTGCATCACAAAGAAAATAATCCCCCAGGTTCGGATTCCCAGGGCTCTGTATGTGGAGCT 1837

Qy        157 GACAGACCCAAGGACAGAACACAGCAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCC 216
              ||||||||  ||| ||| | | ||||||||||||| || |||| |   |||  ||| |||
Db       1838 GACAGACCTGAGGCCAGGAGATAGCAGAGGTCAGCCCTAGGGAGGGTGGGTCATCCACCC 1897

Qy        217 AGGGGATGGGGGTCCATCCACCTTGC 242
              ||||||  ||||| || |  ||||||
Db       1898 AGGGGACAGGGGTGCACCAGCCTTGC 1923


RESULT 12
US-08-481-968A-5
; Sequence 5, Application US/08481968A
; Patent No. 6300490
; GENERAL INFORMATION:
;  APPLICANT:  Huber, Brian
;  APPLICANT:  Richards, Cynthia
;  TITLE OF INVENTION:  Molecular Constructs Comprising a Carcinoembryonic Antigen (CEA
;  TITLE OF INVENTION:  Transcriptional Regulatory Region
;  FILE REFERENCE:  PB1087US4
;  CURRENT APPLICATION NUMBER: US/08/481,968A
;  CURRENT FILING DATE:  1998-06-07
;  NUMBER OF SEQ ID NOS:  36
;  SOFTWARE:  PatentIn version 3.0
; SEQ ID NO 5
;  LENGTH: 3774
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-08-481-968A-5

  Query Match             19.9%;  Score 94;  DB 3;  Length 3774;
  Best Local Similarity   69.5%;  Pred. No. 1.7e-18;
  Matches  185;  Conservative    0;  Mismatches   50;  Indels   31;  Gaps    3;

Qy          4 CACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTGGGC 63
              ||  |  ||||||||   | || |||||||||||||||||||||||||||||| |||||
Db       1662 CAGTAAACAGTGAGCTCCTATCCAGCCCCCAGAGCCACCTCTGTCACCTTCCTGCTGGGC 1721

Qy         64 ATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGGTTT 123
              ||||||||||||| || ||| ||  |||||||||||||||| ||   |  ||||||||
Db       1722 ATCATCCCACCTTCACA-AGCACTAAAGAGCATGGGGAGACCTGG---CTAGCTGGGTTT 1777

Qy        124 CTCTGTCACAAAGGAAAATAATCCCCCTGGT--------------------------GT 156
              ||   |||||||| |||  |  ||||  | |                          |
Db       1778 CTGCATCACAAAGAAAATAATCCCCCAGGTTCGGATTCCCAGGGCTCTGTATGTGGAGCT 1837

Qy        157 GACAGACCCAAGGACAGAACACAGCAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCC 216
              ||||||||  ||| ||| | | ||||||||||||| || |||| |   |||  ||| |||
Db       1838 GACAGACCTGAGGCCAGGAGATAGCAGAGGTCAGCCCTAGGGAGGGTGGGTCATCCACCC 1897

Qy        217 AGGGGATGGGGGTCCATCCACCTTGC 242
              ||||||  ||||| || |  ||||||
Db       1898 AGGGGACAGGGGTGCACCAGCCTTGC 1923


RESULT 13
US-08-154-712B-5
; Sequence 5, Application US/08154712B
; Patent No. 6337209
; GENERAL INFORMATION:
;  APPLICANT:  Huber, Brian
;  APPLICANT:  Richards, Cynthia
;  TITLE OF INVENTION:  Molecular Constructs Containing a Carcinoembryonic Antigen Regu
;  TITLE OF INVENTION:  Sequence
;  FILE REFERENCE:  PB1087US3
;  CURRENT APPLICATION NUMBER: US/08/154,712B
;  CURRENT FILING DATE:  1993-11-19
;  NUMBER OF SEQ ID NOS:  36
;  SOFTWARE:  PatentIn version 3.0
; SEQ ID NO 5
;  LENGTH: 3774
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-08-154-712B-5

  Query Match             19.9%;  Score 94;  DB 3;  Length 3774;
  Best Local Similarity   69.5%;  Pred. No. 1.7e-18;
  Matches  185;  Conservative    0;  Mismatches   50;  Indels   31;  Gaps    3;

Qy          4 CACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTGGGC 63
              ||  |  ||||||||   | || |||||||||||||||||||||||||||||| |||||
Db       1662 CAGTAAACAGTGAGCTCCTATCCAGCCCCCAGAGCCACCTCTGTCACCTTCCTGCTGGGC 1721

Qy         64 ATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGGTTT 123
              ||||||||||||| || ||| ||  |||||||||||||||| ||   |  ||||||||
Db       1722 ATCATCCCACCTTCACA-AGCACTAAAGAGCATGGGGAGACCTGG---CTAGCTGGGTTT 1777

Qy        124 CTCTGTCACAAAGGAAAATAATCCCCCTGGT--------------------------GT 156
              ||   |||||||| |||  |  ||||  | |                          |
Db       1778 CTGCATCACAAAGAAAATAATCCCCCAGGTTCGGATTCCCAGGGCTCTGTATGTGGAGCT 1837

Qy        157 GACAGACCCAAGGACAGAACACAGCAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCC 216
              ||||||||  ||| ||| | | ||||||||||||| || |||| |   |||  ||| |||
Db       1838 GACAGACCTGAGGCCAGGAGATAGCAGAGGTCAGCCCTAGGGAGGGTGGGTCATCCACCC 1897

Qy        217 AGGGGATGGGGGTCCATCCACCTTGC 242
              ||||||  ||||| || |  ||||||
Db       1898 AGGGGACAGGGGTGCACCAGCCTTGC 1923


RESULT 14
US-09-947-925A-5
; Sequence 5, Application US/09947925A
; Patent No. 6699690
; GENERAL INFORMATION:
;  APPLICANT: Huber, Brian
;  APPLICANT:  Richards, Cynthia
;  TITLE OF INVENTION: Molecular Constructs Containing a Carcinoembryonic
;  TITLE OF INVENTION:  Antigen Regulatory
;  TITLE OF INVENTION:  Sequence
;  FILE REFERENCE: PB1087US3
;  CURRENT APPLICATION NUMBER: US/09/947,925A
;  CURRENT FILING DATE:  2001-09-06
;  PRIOR APPLICATION NUMBER: US/08/154,712
;  PRIOR FILING DATE: 1993-11-19
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
;  LENGTH: 3774
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-09-947-925A-5

  Query Match             19.9%;  Score 94;  DB 4;  Length 3774;
  Best Local Similarity   69.5%;  Pred. No. 1.7e-18;
  Matches  185;  Conservative    0;  Mismatches   50;  Indels   31;  Gaps    3;

Qy          4 CACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTGGGC 63
              ||  |  ||||||||   | || |||||||||||||||||||||||||||||| |||||
Db       1662 CAGTAAACAGTGAGCTCCTATCCAGCCCCCAGAGCCACCTCTGTCACCTTCCTGCTGGGC 1721

Qy         64 ATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGGTTT 123
              ||||||||||||| || ||| ||  |||||||||||||||| ||   |  ||||||||
Db       1722 ATCATCCCACCTTCACA-AGCACTAAAGAGCATGGGGAGACCTGG---CTAGCTGGGTTT 1777

Qy        124 CTCTGTCACAAAGGAAAATAATCCCCCTGGT--------------------------GT 156
              ||   |||||||| |||  |  ||||  | |                          |
Db       1778 CTGCATCACAAAGAAAATAATCCCCCAGGTTCGGATTCCCAGGGCTCTGTATGTGGAGCT 1837
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Qy        157 GACAGACCCAAGGACAGAACACAGCAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCC 216
              ||||||||  ||| ||| | | |||||||||||||| || |||| |   |||  ||| |||
Db       1838 GACAGACCTGAGGCCAGGAGATAGCAGAGGTCAGCCCTAGGGAGGGTGGGTCATCCACCC 1897

Qy        217 AGGGGATGGGGGTCCATCCACCTTGC 242
              ||||||  |||||  || |  ||||||
Db       1898 AGGGGACAGGGGTGCACCAGCCTTGC 1923


RESULT 15
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
;  GENERAL INFORMATION:
;    APPLICANT:  DORNER, F.
;    APPLICANT:  SCHEIFLINGER, F.
;    APPLICANT:  FALKNER, F. G.
;    TITLE OF INVENTION:  RECOMBINANT FOWLPOX VIRUS
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  1800 Diagonal Road, Suite 500
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22313-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/232,463
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/935,313
;      FILING DATE:
;      APPLICATION NUMBER:  EP 91 114 300.6
;      FILING DATE:  26-AUG-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  30472/114 IMMU
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)836-9300
;      TELEFAX:  (703)683-4109
;      TELEX:  899149
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7218 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      CLONE:  pTZgpt-F1s
US-08-232-463-14

  Query Match             15.1%;  Score 71.2;  DB 1;  Length 7218;
  Best Local Similarity   4.0%;  Pred. No. 1.9e-11;
  Matches   16;  Conservative  236;  Mismatches  144;  Indels    0;  Gaps    0;

Qy         76 TCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGGTTTCTCTGTCACAAA 135
              | | ::::    :::::: : :::::::   ::::    :  :::       :  : :::
Db       1437 TACRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1378

Qy        136 GGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAGCAGAGGTCAGCACTG 195
              :::::: ::       :: : :: :::   ::::: :::: : :: :::::  :: :  :
Db       1377 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1318

Qy        196 GGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTTGCCGAAAAGATTTGT 255
              ::::::: :::  :       :::::: :::::   :   :    :  :::::::   :

Db       1317 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1258

Qy        256 CTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGAGGCAGAAATGAGAGG 315
              :::::: :::::: :::::::::::::::::::::::: :::::::: ::::: ::::::
Db       1257 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1198

Qy        316 GGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCACGTGATGCTGAGAAG 375
              :::::::: :::::: :   ::: :::::  : :   : ::   : : :: :  ::::::
Db       1197 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1138

Qy        376 TACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACAGCAGACCAGACAGTC 435
              :    :    :::::::::   :::: :::::::::::::: :: :::  ::: ::
Db       1137 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1078

Qy        436 ACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 471
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Db       1077 RRRRRRRRRRRATCGCAAGCTCCCTCGACCTGCAGC 1042


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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

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(without alignments)
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Perfect score: 472
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4085731 seqs, 2756760397 residues

Total number of hits satisfying chosen parameters: 8171462

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	472	100.0	472	10	US-09-151-376-54	Sequence 54, Appl
3	472	100.0	472	14	US-10-045-116-1	Sequence 1, Appli
4	472	100.0	472	15	US-10-139-089-7	Sequence 7, Appli
5	472	100.0	472	15	US-10-139-089-54	Sequence 54, Appl
6	472	100.0	472	18	US-10-822-873-7	Sequence 7, Appli
7	472	100.0	472	18	US-10-822-873-54	Sequence 54, Appl
8	471	99.8	11288	9	US-09-947-925A-4	Sequence 4, Appli
9	471	99.8	11288	9	US-09-822-634-1	Sequence 1, Appli
10	471	99.8	15056	9	US-09-392-822-4	Sequence 4, Appli
11	471	99.8	15056	10	US-09-814-357-14	Sequence 14, Appl
12	471	99.8	15056	10	US-09-814-351-14	Sequence 14, Appl
13	471	99.8	15056	14	US-10-045-116-25	Sequence 25, Appl
14	471	99.8	15056	15	US-10-226-820-10	Sequence 10, Appl
15	432.4	91.6	3281	15	US-10-090-238-1	Sequence 1, Appli
16	350.4	74.2	425	14	US-10-212-667-2	Sequence 2, Appli
17	156.6	33.2	2073	9	US-09-924-103-1	Sequence 1, Appli
18	120.8	25.6	1855	13	US-10-027-632-97812	Sequence 97812, A
19	120.8	25.6	1855	15	US-10-027-632-97812	Sequence 97812, A
20	99.2	21.0	608	13	US-10-027-632-8715	Sequence 8715, Ap
21	99.2	21.0	608	15	US-10-027-632-8715	Sequence 8715, Ap
22	94	19.9	3774	9	US-09-947-925A-5	Sequence 5, Appli
23	75	15.9	2974	9	US-09-954-456-56	Sequence 56, Appl
24	75	15.9	2974	9	US-09-880-107-2317	Sequence 2317, Ap
25	75	15.9	2974	15	US-10-157-031-340	Sequence 340, App
26	75	15.9	2974	15	US-10-207-655-86	Sequence 86, Appl
27	75	15.9	2974	15	US-10-117-937-593	Sequence 593, App
28	75	15.9	2974	15	US-10-295-027-331	Sequence 331, App
29	75	15.9	2974	16	US-10-240-425-1314	Sequence 1314, Ap
30	75	15.9	2974	17	US-10-734-564-5	Sequence 5, Appli
31	75	15.9	2974	17	US-10-657-022-89	Sequence 89, Appl
32	75	15.9	2975	14	US-10-090-326-1	Sequence 1, Appli
33	69.4	14.7	653	11	US-09-969-034-4281	Sequence 4281, Ap
34	67.8	14.4	2547	10	US-09-814-353-20321	Sequence 20321, A
35	60.6	12.8	474	9	US-09-864-761-6512	Sequence 6512, Ap
36	59	12.5	1298	9	US-09-925-301-290	Sequence 290, App
37	57.6	12.2	387	9	US-09-738-973-177	Sequence 177, App
38	57.6	12.2	387	9	US-09-854-133-177	Sequence 177, App
39	57.6	12.2	387	15	US-10-144-649A-177	Sequence 177, App
40	57.2	12.1	460	9	US-09-922-217-169	Sequence 169, App
41	57.2	12.1	460	9	US-09-833-263-169	Sequence 169, App
42	57.2	12.1	460	13	US-10-025-380-169	Sequence 169, App
c 43	56	11.9	676	13	US-10-027-632-127633	Sequence 127633,
c 44	56	11.9	676	15	US-10-027-632-127633	Sequence 127633,
c 45	55.4	11.7	294	9	US-09-920-300A-311	Sequence 311, App

ALIGNMENTS

RESULT 1
US-09-151-376-7
; Sequence 7, Application US/09151376
; Publication No. US20030044383A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, D.R.
; APPLICANT: Schuur, E.R.
; TITLE OF INVENTION: TISSUE SPECIFIC VIRAL VECTORS
; FILE REFERENCE: 348022000221
; CURRENT APPLICATION NUMBER: US/09/151,376
; CURRENT FILING DATE: 1998-09-10
; EARLIER APPLICATION NUMBER: 08/669,753
; EARLIER FILING DATE: 1996-06-26
; EARLIER APPLICATION NUMBER: 08/495,034
; EARLIER FILING DATE: 1995-06-27
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 472
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-151-376-7

Query Match 100.0%; Score 472; DB 10; Length 472;
Best Local Similarity 100.0%; Pred. No. 2.8e-136;
Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
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Db          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60

Qy         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
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Db         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
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Qy        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
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Db        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180

Qy        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240

Qy        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300
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Db        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300

Qy        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360
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Db        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360

Qy        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420

Qy        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGCA 472
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Db        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGCA 472
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RESULT 2
US-09-151-376-54
; Sequence 54, Application US/09151376
; Publication No. US20030044383A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, D.R.
; APPLICANT: Schuur, E.R.
; TITLE OF INVENTION: TISSUE SPECIFIC VIRAL VECTORS
; FILE REFERENCE: 348022000221
; CURRENT APPLICATION NUMBER: US/09/151,376
; CURRENT FILING DATE: 1998-09-10
; EARLIER APPLICATION NUMBER: 08/669,753
; EARLIER FILING DATE: 1996-06-26
; EARLIER APPLICATION NUMBER: 08/495,034
; EARLIER FILING DATE: 1995-06-27
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 54
; LENGTH: 472
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Unknown
US-09-151-376-54

Query Match 100.0%; Score 472; DB 10; Length 472;
Best Local Similarity 100.0%; Pred. No. 2.8e-136;
Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
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Db          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60

Qy         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
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Db         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120

Qy        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180

Qy        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240

Qy        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300

Qy        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360

Qy        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420

Qy        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGCA 472
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Db        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGCA 472
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RESULT 3
US-10-045-116-1
; Sequence 1, Application US/10045116
; Publication No. US20030026792A1
; GENERAL INFORMATION:
; APPLICANT: Lamparski, Henry
; Schuur, Eric
; Henderson, Daniel
; TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC FOR CELLS
; EXPRESSING CARCINOEMBRYONIC ANTIGENS AND METHODS OF USE
; THEREOF
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/045,116
; FILING DATE: 23-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/033,555A
; FILING DATE: 02-Mar-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: POLIZZI, CATHERINE M.
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 34802-30005.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141 MRSNFOERS SFO
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 472 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-045-116-1

Query Match 100.0%; Score 472; DB 14; Length 472;
Best Local Similarity 100.0%; Pred. No. 2.8e-136;
Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
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Db          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60

Qy         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
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Qy        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180

Qy        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240

Qy        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300

Qy        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360

Qy        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420

Qy        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGCA 472
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Db        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGCA 472
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RESULT 4
US-10-139-089-7
; Sequence 7, Application US/10139089
; Publication No. US20030152553A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, D.R.
; APPLICANT: Schuur, E.R.
; TITLE OF INVENTION: TISSUE SPECIFIC VIRAL VECTORS
; FILE REFERENCE: 348022000221
; CURRENT APPLICATION NUMBER: US/10/139,089
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: 08/669,753
; PRIOR FILING DATE: 1996-06-26
; PRIOR APPLICATION NUMBER: 08/495,034
; PRIOR FILING DATE: 1995-06-27
; PRIOR APPLICATION NUMBER: 09/509,591
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: 09/151,376
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 09/033,428
; PRIOR FILING DATE: 1998-03-02
; PRIOR APPLICATION NUMBER: 60/039,597
; PRIOR FILING DATE: 1997-03-03
; PRIOR APPLICATION NUMBER: 09/033,555
; PRIOR FILING DATE: 1998-03-02
; PRIOR APPLICATION NUMBER: 60/039,763
; PRIOR FILING DATE: 1997-03-03
; PRIOR APPLICATION NUMBER: 09/033,333
; PRIOR FILING DATE: 1998-03-02
; PRIOR APPLICATION NUMBER: 60/039,762
; PRIOR FILING DATE: 1997-03-03
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 472
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-139-089-7

Query Match 100.0%; Score 472; DB 15; Length 472;
Best Local Similarity 100.0%; Pred. No. 2.8e-136;
Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
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Db          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
```

```
Qy         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
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Db         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120

Qy        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
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Db        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180

Qy        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240
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Db        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240

Qy        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300
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Db        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300

Qy        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360
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Db        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360

Qy        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420

Qy        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGCA 472
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Db        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGCA 472
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RESULT 5
US-10-139-089-54
; Sequence 54, Application US/10139089
; Publication No. US20030152553A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, D.R.
; APPLICANT: Schuur, E.R.
; TITLE OF INVENTION: TISSUE SPECIFIC VIRAL VECTORS
; FILE REFERENCE: 348022000221
; CURRENT APPLICATION NUMBER: US/10/139,089
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: 08/669,753
; PRIOR FILING DATE: 1996-06-26
; PRIOR APPLICATION NUMBER: 08/495,034
; PRIOR FILING DATE: 1995-06-27
; PRIOR APPLICATION NUMBER: 09/509,591
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: 09/151,376
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 09/033,428
; PRIOR FILING DATE: 1998-03-02
; PRIOR APPLICATION NUMBER: 60/039,597
; PRIOR FILING DATE: 1997-03-03
; PRIOR APPLICATION NUMBER: 09/033,555
; PRIOR FILING DATE: 1998-03-02
; PRIOR APPLICATION NUMBER: 60/039,763
; PRIOR FILING DATE: 1997-03-03
; PRIOR APPLICATION NUMBER: 09/033,333
; PRIOR FILING DATE: 1998-03-02
; PRIOR APPLICATION NUMBER: 60/039,762
; PRIOR FILING DATE: 1997-03-03
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 54
; LENGTH: 472
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Unknown
US-10-139-089-54

Query Match 100.0%; Score 472; DB 15; Length 472;
Best Local Similarity 100.0%; Pred. No. 2.8e-136;
Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
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Qy         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
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Db         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120

Qy        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
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Db        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180

Qy        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240
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Db        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240

Qy        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300
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Db        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300

Qy        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360
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Db        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360

Qy        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420

Qy        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGCA 472
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGCA 472
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RESULT 6
US-10-822-873-7
; Sequence 7, Application US/10822873
; Publication No. US20040241857A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, D.R.
; APPLICANT: Schuur, E.R.
; TITLE OF INVENTION: TISSUE SPECIFIC ADENOVIRAL VECTORS
; FILE REFERENCE: CELL-004CON2
; CURRENT APPLICATION NUMBER: US/10/822,873
; CURRENT FILING DATE: 2004-04-13
; PRIOR APPLICATION NUMBER: 09/732,169
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: 09/151,376
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 08/669,753
; PRIOR FILING DATE: 1996-06-26
; PRIOR APPLICATION NUMBER: 08/495,034
; PRIOR FILING DATE: 1995-06-27
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 472
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-822-873-7

Query Match 100.0%; Score 472; DB 18; Length 472;
Best Local Similarity 100.0%; Pred. No. 2.8e-136;
Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60

Qy         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120

Qy        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180

Qy        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240

Qy        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300

Qy        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360

Qy        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420

Qy        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGCA 472
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGCA 472
```

RESULT 7
US-10-822-873-54
; Sequence 54, Application US/10822873
; Publication No. US20040241857A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, D.R.
; APPLICANT: Schuur, E.R.
; TITLE OF INVENTION: TISSUE SPECIFIC ADENOVIRAL VECTORS
; FILE REFERENCE: CELL-004CON2
; CURRENT APPLICATION NUMBER: US/10/822,873
; CURRENT FILING DATE: 2004-04-13
; PRIOR APPLICATION NUMBER: 09/732,169
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: 09/151,376
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 08/669,753
; PRIOR FILING DATE: 1996-06-26
; PRIOR APPLICATION NUMBER: 08/495,034
; PRIOR FILING DATE: 1995-06-27
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 54
; LENGTH: 472
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Unknown
US-10-822-873-54

Query Match 100.0%; Score 472; DB 18; Length 472;
Best Local Similarity 100.0%; Pred. No. 2.8e-136;
Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60

Qy         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120

Qy        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180

Qy        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240
```

```
Qy        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300

Qy        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360

Qy        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420

Qy        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGCA 472
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGCA 472


RESULT 8
US-09-947-925A-4
; Sequence 4, Application US/09947925A
; Patent No. US20020055482A1
; GENERAL INFORMATION:
;  APPLICANT: Huber, Brian
;  APPLICANT:  Richards, Cynthia
;  TITLE OF INVENTION: Molecular Constructs Containing a Carcinoembryonic
;  TITLE OF INVENTION:  Antigen Regulatory
;  TITLE OF INVENTION:  Sequence
;  FILE REFERENCE: PB1087US3
;  CURRENT APPLICATION NUMBER: US/09/947,925A
;  CURRENT FILING DATE:  2001-09-06
;  PRIOR APPLICATION NUMBER: US/08/154,712
;  PRIOR FILING DATE: 1993-11-19
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
;   LENGTH: 11288
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-947-925A-4

  Query Match             99.8%;  Score 471;  DB 9;  Length 11288;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-135;
  Matches  471;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10294 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 10353

Qy         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10354 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 10413

Qy        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10414 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 10473

Qy        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10474 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 10533

Qy        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10534 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 10593

Qy        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10594 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 10653

Qy        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10654 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 10713

Qy        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10714 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 10764


RESULT 9
US-09-822-634-1
; Sequence 1, Application US/09822634
; Patent No. US20020150556A1
; GENERAL INFORMATION:
;  APPLICANT: Vile, Richard G.
;  APPLICANT:  Harrington, Kevin
;  APPLICANT:  Bateman, Andrew
;  APPLICANT:  Murphy, Steven
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TISSUE
;  TITLE OF INVENTION:  SPECIFIC GENE REGULATION THERAPY
;  FILE REFERENCE: 07039-289001
;  CURRENT APPLICATION NUMBER: US/09/822,634
;  CURRENT FILING DATE:  2001-03-30
;  PRIOR APPLICATION NUMBER: 60/193,977
;  PRIOR FILING DATE: 2000-03-31
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 11288
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (10804)...(10935)
US-09-822-634-1

  Query Match             99.8%;  Score 471;  DB 9;  Length 11288;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-135;
  Matches  471;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10294 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 10353

Qy         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10354 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 10413

Qy        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10414 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 10473

Qy        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10474 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 10533

Qy        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10534 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 10593

Qy        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10594 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 10653

Qy        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10654 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 10713

Qy        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10714 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 10764


RESULT 10
US-09-392-822-4
; Sequence 4, Application US/09392822
; Patent No. US20010053352A1
```

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; GENERAL INFORMATION:
;  APPLICANT: Yu, De Chao
;  APPLICANT: Henderson, Daniel
;  TITLE OF INVENTION: Adenovirus Vectors Containing Cell
;  TITLE OF INVENTION: Status-Specific Response Elements and Methods of Use Thereof
;  FILE REFERENCE: 348022001200
;  CURRENT APPLICATION NUMBER: US/09/392,822
;  CURRENT FILING DATE: 1999-09-09
;  EARLIER APPLICATION NUMBER: 60/099,791
;  EARLIER FILING DATE: 1998-09-10
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
;   LENGTH: 15056
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-09-392-822-4

  Query Match             99.8%;  Score 471;  DB 9;  Length 15056;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-135;
  Matches  471;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14062 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 14121

Qy         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14122 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 14181

Qy        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14182 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 14241

Qy        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14242 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 14301

Qy        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14302 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 14361

Qy        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14362 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 14421

Qy        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14422 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 14481

Qy        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14482 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 14532


RESULT 11
US-09-814-357-14
; Sequence 14, Application US/09814357
; Publication No. US20030068307A1
; GENERAL INFORMATION:
;  APPLICANT: Yu, De-Chao
;  APPLICANT:  Chen, Yu
;  APPLICANT:  Henderson, Daniel R.
;  TITLE OF INVENTION: METHODS OF TREATING NEOPLASIA
;  TITLE OF INVENTION:  WITH COMBINATION TARGET CELL-SPECIFIC ADENOVIRUS,
;  TITLE OF INVENTION:  CHEMOTHERAPY AND RADIATION
;  FILE REFERENCE: 348022001600
;  CURRENT APPLICATION NUMBER: US/09/814,357
;  CURRENT FILING DATE:  2001-10-15
;  PRIOR APPLICATION NUMBER: 60/192,015
;  PRIOR FILING DATE: 2000-03-24
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
;   LENGTH: 15056
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: CEA TRE
US-09-814-357-14

  Query Match             99.8%;  Score 471;  DB 10;  Length 15056;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-135;
  Matches  471;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14062 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 14121

Qy         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14122 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 14181

Qy        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14182 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 14241

Qy        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14242 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 14301

Qy        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14302 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 14361

Qy        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14362 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 14421

Qy        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14422 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 14481

Qy        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14482 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 14532


RESULT 12
US-09-814-351-14
; Sequence 14, Application US/09814351
; Publication No. US20030148520A1
; GENERAL INFORMATION:
;  APPLICANT: Yu, De-Chao
;  APPLICANT:  Li, Yuanhao
;  APPLICANT:  Henderson, Daniel R.
;  TITLE OF INVENTION: CELL-SPECIFIC ADENOVIRUS VECTORS
;  TITLE OF INVENTION:  COMPRISING AN INTERNAL RIBOSOME ENTRY SITE
;  FILE REFERENCE: 348022001700
;  CURRENT APPLICATION NUMBER: US/09/814,351
;  CURRENT FILING DATE:  2001-03-21
;  PRIOR APPLICATION NUMBER: 60/192,156
;  PRIOR FILING DATE: 2000-03-24
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
;   LENGTH: 15056
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: CEA TRE
US-09-814-351-14

  Query Match             99.8%;  Score 471;  DB 10;  Length 15056;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-135;
  Matches  471;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14062 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 14121

Qy         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14122 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 14181

Qy        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14182 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 14241

Qy        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14242 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 14301

Qy        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14302 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 14361

Qy        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14362 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 14421

Qy        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14422 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 14481

Qy        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14482 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 14532
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RESULT 13
US-10-045-116-25
; Sequence 25, Application US/10045116
; Publication No. US20030026792A1
;   GENERAL INFORMATION:
;        APPLICANT: Lamparski, Henry
;                   Schuur, Eric
;                   Henderson, Daniel
;        TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC FOR CELLS
;                            EXPRESSING CARCINOEMBRYONIC ANTIGENS AND METHODS OF USE
;                            THEREOF
;        NUMBER OF SEQUENCES: 25
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: MORRISON & FOERSTER
;             STREET: 755 PAGE MILL ROAD
;             CITY: PALO ALTO
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 94304-1018
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/045,116
;             FILING DATE: 23-Oct-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/033,555A
;             FILING DATE: 02-Mar-1998
;        ATTORNEY/AGENT INFORMATION:
;             NAME: POLIZZI, CATHERINE M.
;             REGISTRATION NUMBER: 40,130
;             REFERENCE/DOCKET NUMBER: 34802-30005.00
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 813-5600
;             TELEFAX: (415) 494-0792
;             TELEX: 706141 MRSNFOERS SFO
;   INFORMATION FOR SEQ ID NO: 25:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 15056 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-10-045-116-25

  Query Match             99.8%;  Score 471;  DB 14;  Length 15056;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-135;
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Qy         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
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; Sequence 10, Application US/10226820
; Publication No. US20030118555A1
; GENERAL INFORMATION:
;  APPLICANT: Henderson, Daniel R.
;  APPLICANT:  Yu, De Chao
;  TITLE OF INVENTION: TARGET CELL-SPECIFIC ADENOVIRAL VECTORS
;  TITLE OF INVENTION:  CONTAINING E3 AND METHODS OF USE THEREOF
;  FILE REFERENCE: 348022001300
;  CURRENT APPLICATION NUMBER: US/10/226,820
;  CURRENT FILING DATE:  2002-08-21
;  PRIOR APPLICATION NUMBER: US/09/474,699
;  PRIOR FILING DATE: 1999-12-29
;  PRIOR APPLICATION NUMBER: 60/114,262
;  PRIOR FILING DATE: 1998-12-30
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
;   LENGTH: 15056
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-10-226-820-10

  Query Match             99.8%;  Score 471;  DB 15;  Length 15056;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-135;
  Matches  471;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 471
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RESULT 15
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; Sequence 1, Application US/10090238
; Publication No. US20030176377A1
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute
; APPLICANT: Rong Xiang
; APPLICANT: Ralph A. Reisfeld
; TITLE OF INVENTION: DNA VACCINES ENCODING CEA AND A CD40
; TITLE OF INVENTION: LIGAND AND METHODS OF USE THEREOF
; FILE REFERENCE: TSRI-830.0
; CURRENT APPLICATION NUMBER: US/10/090,238
; CURRENT FILING DATE: 2002-03-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3281
; TYPE: DNA
; ORGANISM: human
US-10-090-238-1

Query Match 91.6%; Score 432.4; DB 15; Length 3281;
Best Local Similarity 98.9%; Pred. No. 9.8e-124;
Matches 467; Conservative 0; Mismatches 1; Indels 4; Gaps 3;

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Job time : 455 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 11, 2004, 06:53:29 ; Search time 3792 Seconds
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Title: US-10-045-116-1
Perfect score: 472
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Scoring table: IDENTITY_NUC
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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9	471	99.8	3500	54	US-10-486-319B-11	Sequence 11, Appl
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18	471	99.8	15056	34	US-09-814-357-14	Sequence 14, Appl
19	471	99.8	15056	45	US-10-045-116-25	Sequence 25, Appl
20	471	99.8	15056	49	US-10-226-820-10	Sequence 10, Appl
21	471	99.8	15056	57	US-10-691-045-14	Sequence 14, Appl
22	471	99.8	15056	64	US-10-938-227-3	Sequence 3, Appli
23	471	99.8	25321	40	US-09-949-016-12355	Sequence 12355, A
24	471	99.8	25321	40	US-09-949-016-14039	Sequence 14039, A
25	471	99.8	25321	64	US-10-940-774-12355	Sequence 12355, A
26	471	99.8	25321	64	US-10-940-774-14039	Sequence 14039, A
c 27	471	99.8	5401257	40	US-09-947-916-209	Sequence 209, App
28	432.4	91.6	3281	2	PCT-US03-06295-1	Sequence 1, Appli
29	432.4	91.6	3281	46	US-10-090-238-1	Sequence 1, Appli
30	432.4	91.6	5346	98	US-60-324-185-26827	Sequence 26827, A
31	432.4	91.6	5779	82	US-60-172-373-8089	Sequence 8089, Ap
32	350.4	74.2	425	2	PCT-US02-24741-2	Sequence 2, Appli
33	350.4	74.2	425	49	US-10-212-667-2	Sequence 2, Appli
34	350.4	74.2	425	97	US-60-310-905-2	Sequence 2, Appli
35	278.2	58.9	3500	54	US-10-486-319A-52	Sequence 52, Appl
36	278.2	58.9	3500	54	US-10-486-319B-52	Sequence 52, Appl
37	271.8	57.6	3500	54	US-10-486-319A-74	Sequence 74, Appl
38	271.8	57.6	3500	54	US-10-486-319B-74	Sequence 74, Appl
39	263.2	55.8	15862	61	US-10-765-790-14	Sequence 14, Appl
40	263.2	55.8	5401257	40	US-09-947-916-209	Sequence 209, App
c 41	263	55.7	3500	54	US-10-486-319A-53	Sequence 53, Appl
c 42	263	55.7	3500	54	US-10-486-319B-53	Sequence 53, Appl
c 43	256.6	54.4	3500	54	US-10-486-319A-75	Sequence 75, Appl
c 44	256.6	54.4	3500	54	US-10-486-319B-75	Sequence 75, Appl
45	156.6	33.2	19272	40	US-09-949-016-13462	Sequence 13462, A

ALIGNMENTS

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RESULT 1
US-09-033-555-1
; Sequence 1, Application US/09033555
;  GENERAL INFORMATION:
;     APPLICANT:  Lamparski, Henry
;     APPLICANT:  Schuur, Eric
;     APPLICANT:  Henderson, Daniel
;     TITLE OF INVENTION:  ADENOVIRUS VECTORS SPECIFIC FOR CELLS
;     TITLE OF INVENTION:  EXPRESSING CARCINOEMBRYONIC ANTIGENS AND METHODS OF USE
;     TITLE OF INVENTION:  THEREOF
;     NUMBER OF SEQUENCES:  20
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  MORRISON & FOERSTER
;       STREET:  755 PAGE MILL ROAD
;       CITY:  PALO ALTO
;       STATE:  CA
;       COUNTRY:  USA
;       ZIP:  94304-1018
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/033,555
;       FILING DATE:
;       CLASSIFICATION:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  POLIZZI, CATHERINE M.
;       REGISTRATION NUMBER:  40,130
;       REFERENCE/DOCKET NUMBER:  34802-30005.00
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (415) 813-5600
;       TELEFAX:  (415) 494-0792
;       TELEX:  706141 MRSNFOERS SFO
;  INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  472 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
US-09-033-555-1

  Query Match             100.0%;  Score 472;  DB 15;  Length 472;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-114;
  Matches  472;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60

Qy         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120

Qy        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180

Qy        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240

Qy        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300

Qy        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360

Qy        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420

Qy        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGCA 472
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Db        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGCA 472

RESULT 2
US-09-033-555A-1
; Sequence 1, Application US/09033555A
;   GENERAL INFORMATION:
;        APPLICANT: Lamparski, Henry
;                   Schuur, Eric
;                   Henderson, Daniel
;        TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC FOR CELLS
;                            EXPRESSING CARCINOEMBRYONIC ANTIGENS AND METHODS OF USE
;                            THEREOF
;        NUMBER OF SEQUENCES: 25
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: MORRISON & FOERSTER
;             STREET: 755 PAGE MILL ROAD
;             CITY: PALO ALTO
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 94304-1018
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/033,555A
;             FILING DATE: 02-Mar-1998
;             CLASSIFICATION: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: POLIZZI, CATHERINE M.
;             REGISTRATION NUMBER: 40,130
;             REFERENCE/DOCKET NUMBER: 34802-30005.00
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 813-5600
;             TELEFAX: (415) 494-0792
;             TELEX: 706141 MRSNFOERS SFO
;   INFORMATION FOR SEQ ID NO: 1:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 472 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-033-555A-1

  Query Match             100.0%;  Score 472;  DB 15;  Length 472;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-114;
  Matches  472;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60

Qy         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120

Qy        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180

Qy        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240

Qy        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300

Qy        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360

Qy        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420

Qy        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGCA 472
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGCA 472


RESULT 3
US-10-045-116-1
; Sequence 1, Application US/10045116
;   GENERAL INFORMATION:
;        APPLICANT: Lamparski, Henry
;                   Schuur, Eric
;                   Henderson, Daniel
;        TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC FOR CELLS
;                            EXPRESSING CARCINOEMBRYONIC ANTIGENS AND METHODS OF USE
;                            THEREOF
;        NUMBER OF SEQUENCES: 25
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: MORRISON & FOERSTER
;             STREET: 755 PAGE MILL ROAD
;             CITY: PALO ALTO
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 94304-1018
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/045,116
;             FILING DATE: 23-Oct-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/033,555A
;             FILING DATE: 02-Mar-1998
;        ATTORNEY/AGENT INFORMATION:
;             NAME: POLIZZI, CATHERINE M.
;             REGISTRATION NUMBER: 40,130
;             REFERENCE/DOCKET NUMBER: 34802-30005.00
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 813-5600
;             TELEFAX: (415) 494-0792
;             TELEX: 706141 MRSNFOERS SFO
;   INFORMATION FOR SEQ ID NO: 1:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 472 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-045-116-1

  Query Match             100.0%;  Score 472;  DB 45;  Length 472;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-114;
  Matches  472;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60

Qy         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120

Qy        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
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Qy        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240

Qy        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300

Qy        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360

Qy        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420

Qy        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGCA 472
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Db        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGCA 472
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RESULT 4
US-10-139-089-7
; Sequence 7, Application US/10139089
; GENERAL INFORMATION:
;  APPLICANT: Henderson, D.R.
;  APPLICANT:  Schuur, E.R.
;  TITLE OF INVENTION: TISSUE SPECIFIC VIRAL VECTORS
;  FILE REFERENCE: 348022000221
;  CURRENT APPLICATION NUMBER: US/10/139,089
;  CURRENT FILING DATE:  2002-05-02
;  PRIOR APPLICATION NUMBER: 08/669,753
;  PRIOR FILING DATE: 1996-06-26
;  PRIOR APPLICATION NUMBER: 08/495,034
;  PRIOR FILING DATE: 1995-06-27
;  PRIOR APPLICATION NUMBER: 09/509,591
;  PRIOR FILING DATE: 2000-06-02
;  PRIOR APPLICATION NUMBER: 09/151,376
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 09/033,428
;  PRIOR FILING DATE: 1998-03-02
;  PRIOR APPLICATION NUMBER: 60/039,597
;  PRIOR FILING DATE: 1997-03-03
;  PRIOR APPLICATION NUMBER: 09/033,555
;  PRIOR FILING DATE: 1998-03-02
;  PRIOR APPLICATION NUMBER: 60/039,763
;  PRIOR FILING DATE: 1997-03-03
;  PRIOR APPLICATION NUMBER: 09/033,333
;  PRIOR FILING DATE: 1998-03-02
;  PRIOR APPLICATION NUMBER: 60/039,762
;  PRIOR FILING DATE: 1997-03-03
;  NUMBER OF SEQ ID NOS: 71
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
;   LENGTH: 472
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-139-089-7

  Query Match             100.0%;  Score 472;  DB 47;  Length 472;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-114;
  Matches  472;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60

Qy         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120

Qy        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180

Qy        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240

Qy        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300

Qy        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360

Qy        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420

Qy        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGCA 472
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Db        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGCA 472
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RESULT 5
US-10-139-089-54
; Sequence 54, Application US/10139089
; GENERAL INFORMATION:
;  APPLICANT: Henderson, D.R.
;  APPLICANT:  Schuur, E.R.
;  TITLE OF INVENTION: TISSUE SPECIFIC VIRAL VECTORS
;  FILE REFERENCE: 348022000221
;  CURRENT APPLICATION NUMBER: US/10/139,089
;  CURRENT FILING DATE:  2002-05-02
;  PRIOR APPLICATION NUMBER: 08/669,753
;  PRIOR FILING DATE: 1996-06-26
;  PRIOR APPLICATION NUMBER: 08/495,034
;  PRIOR FILING DATE: 1995-06-27
;  PRIOR APPLICATION NUMBER: 09/509,591
;  PRIOR FILING DATE: 2000-06-02
;  PRIOR APPLICATION NUMBER: 09/151,376
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 09/033,428
;  PRIOR FILING DATE: 1998-03-02
;  PRIOR APPLICATION NUMBER: 60/039,597
;  PRIOR FILING DATE: 1997-03-03
;  PRIOR APPLICATION NUMBER: 09/033,555
;  PRIOR FILING DATE: 1998-03-02
;  PRIOR APPLICATION NUMBER: 60/039,763
;  PRIOR FILING DATE: 1997-03-03
;  PRIOR APPLICATION NUMBER: 09/033,333
;  PRIOR FILING DATE: 1998-03-02
;  PRIOR APPLICATION NUMBER: 60/039,762
;  PRIOR FILING DATE: 1997-03-03
;  NUMBER OF SEQ ID NOS: 71
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 54
;   LENGTH: 472
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: Description of Unknown Organism: Unknown
US-10-139-089-54

  Query Match             100.0%;  Score 472;  DB 47;  Length 472;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-114;
  Matches  472;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60

Qy         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120

Qy         121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180

Qy         181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240

Qy         241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300

Qy         301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360

Qy         361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420

Qy         421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGCA 472
                 ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGCA 472


RESULT 6
US-10-822-873-7
; Sequence 7, Application US/10822873
; GENERAL INFORMATION:
;  APPLICANT: Henderson, D.R.
;  APPLICANT:  Schuur, E.R.
;  TITLE OF INVENTION: TISSUE SPECIFIC ADENOVIRAL VECTORS
;  FILE REFERENCE: CELL-004CON2
;  CURRENT APPLICATION NUMBER: US/10/822,873
;  CURRENT FILING DATE:  2004-04-13
;  PRIOR APPLICATION NUMBER: 09/732,169
;  PRIOR FILING DATE: 2000-12-06
;  PRIOR APPLICATION NUMBER: 09/151,376
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 08/669,753
;  PRIOR FILING DATE: 1996-06-26
;  PRIOR APPLICATION NUMBER: 08/495,034
;  PRIOR FILING DATE: 1995-06-27
;  NUMBER OF SEQ ID NOS: 71
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
;   LENGTH: 472
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-822-873-7

  Query Match           100.0%;  Score 472;  DB 62;  Length 472;
  Best Local Similarity  100.0%;  Pred. No. 2.8e-114;
  Matches  472;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60

Qy          61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120

Qy         121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180

Qy         181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240

Qy         241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300

Qy         301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360

Qy         361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420

Qy         421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGCA 472
                 ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGCA 472


RESULT 7
US-10-822-873-54
; Sequence 54, Application US/10822873
; GENERAL INFORMATION:
;  APPLICANT: Henderson, D.R.
;  APPLICANT:  Schuur, E.R.
;  TITLE OF INVENTION: TISSUE SPECIFIC ADENOVIRAL VECTORS
;  FILE REFERENCE: CELL-004CON2
;  CURRENT APPLICATION NUMBER: US/10/822,873
;  CURRENT FILING DATE:  2004-04-13
;  PRIOR APPLICATION NUMBER: 09/732,169
;  PRIOR FILING DATE: 2000-12-06
;  PRIOR APPLICATION NUMBER: 09/151,376
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 08/669,753
;  PRIOR FILING DATE: 1996-06-26
;  PRIOR APPLICATION NUMBER: 08/495,034
;  PRIOR FILING DATE: 1995-06-27
;  NUMBER OF SEQ ID NOS: 71
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 54
;   LENGTH: 472
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: Description of Unknown Organism: Unknown
US-10-822-873-54

  Query Match           100.0%;  Score 472;  DB 62;  Length 472;
  Best Local Similarity  100.0%;  Pred. No. 2.8e-114;
  Matches  472;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60

Qy          61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120

Qy         121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180

Qy         181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240

Qy         241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300

Qy         301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360
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Qy        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420

Qy        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGCA 472
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGCA 472


RESULT 8
US-10-486-319A-11
; Sequence 11, Application US/10486319A
; GENERAL INFORMATION:
;  APPLICANT: Epigenomics AG
;  TITLE OF INVENTION: Method and nucleic acids for the analysis of colon cancer
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/10/486,319A
;  CURRENT FILING DATE:  2004-02-09
;  NUMBER OF SEQ ID NOS: 527
; SEQ ID NO 11
;   LENGTH: 3500
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-10-486-319A-11

  Query Match             99.8%;  Score 471;  DB 54;  Length 3500;
  Best Local Similarity   100.0%;  Pred. No. 9.9e-114;
  Matches  471;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2506 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 2565

Qy         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2566 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 2625

Qy        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2626 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 2685

Qy        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2686 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 2745

Qy        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2746 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 2805

Qy        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2806 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 2865

Qy        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2866 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 2925

Qy        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2926 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 2976


RESULT 9
US-10-486-319B-11
; Sequence 11, Application US/10486319B
; GENERAL INFORMATION:
;  APPLICANT: Epigenomics AG
;  TITLE OF INVENTION: Method and nucleic acids for the analysis of colon cancer
;  FILE REFERENCE: 82196
;  CURRENT APPLICATION NUMBER: US/10/486,319B
;  CURRENT FILING DATE:  2004-02-09
;  NUMBER OF SEQ ID NOS: 527
; SEQ ID NO 11
;   LENGTH: 3500
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-10-486-319B-11

  Query Match             99.8%;  Score 471;  DB 54;  Length 3500;
  Best Local Similarity   100.0%;  Pred. No. 9.9e-114;
  Matches  471;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2506 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 2565

Qy         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2566 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 2625

Qy        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2626 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 2685

Qy        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2686 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 2745

Qy        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2746 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 2805

Qy        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2806 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 2865

Qy        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2866 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 2925

Qy        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2926 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 2976


RESULT 10
PCT-US04-13487-1
; Sequence 1, Application PC/TUS0413487
; GENERAL INFORMATION:
;  APPLICANT: DONG, JIAN-YUN
;  APPLICANT:  RUBINCHIK, SEMYON
;  APPLICANT:  WORARATANADHARM, JAN
;  TITLE OF INVENTION: AN AUTOLOGOUS UPREGULATION MECHANISM ALLOWING OPTIMIZED
;  TITLE OF INVENTION:  CELL TYPE-SPECIFIC AND REGULATED GENE EXPRESSION CELLS
;  FILE REFERENCE: MESC:014WO
;  CURRENT APPLICATION NUMBER: PCT/US04/13487
;  CURRENT FILING DATE:  2004-04-30
;  PRIOR APPLICATION NUMBER: 60/467,171
;  PRIOR FILING DATE: 2003-05-01
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 11288
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (10804)..(10938)
PCT-US04-13487-1

  Query Match             99.8%;  Score 471;  DB 2;  Length 11288;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-113;
  Matches  471;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10294 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 10353

Qy         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10354 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 10413

Qy        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10414 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 10473

Qy        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10474 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 10533

Qy        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10534 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 10593

Qy        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10594 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 10653

Qy        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10654 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 10713

Qy        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 471
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10714 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 10764


RESULT 11
US-07-841-961-6
; Sequence 6, Application US/07841961
;  GENERAL INFORMATION:
;    APPLICANT:  Huber, Brian
;    APPLICANT:  Richards, Cynthia A
;    APPLICANT:  Krenitsky, Thomas A
;    TITLE OF INVENTION:  NOVEL ENTITIES FOR CANCER THERAPY
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Donald Brown; Dike, Bronstein, Roberts &
;      ADDRESSEE:  Cushman
;      STREET:  130 Water Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  US
;      ZIP:  12109-4280
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/841,961
;      FILING DATE:  19920226
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brown, Donald
;      REGISTRATION NUMBER:  20845
;      REFERENCE/DOCKET NUMBER:  40361-CIP2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-523-3400
;      TELEFAX:  617)523)6440
;      TELEX:  200291 STRE UR
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11288 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  10804..10866
;    FEATURE:
;      NAME/KEY:  mat_peptide
;      LOCATION:  10281..11288
US-07-841-961-6

  Query Match             99.8%;  Score 471;  DB 4;  Length 11288;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-113;
  Matches  471;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10294 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 10353

Qy         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10354 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 10413

Qy        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10414 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 10473

Qy        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10474 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 10533

Qy        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10534 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 10593

Qy        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10594 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 10653

Qy        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10654 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 10713

Qy        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 471
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10714 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 10764


RESULT 12
US-08-474-420-4
; Sequence 4, Application US/08474420
;  GENERAL INFORMATION:
;    APPLICANT:  HUBER, BRIAN
;    APPLICANT:  RICHARDS, CYNTHIA A
;    APPLICANT:  AUSTIN, ELIZABETH A
;    TITLE OF INVENTION:  NOVEL ENTITIES FOR CANCER THERAPY
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ROTHWELL, FIGG, ERNST & KURZ, P.C.
;      STREET:  SUITE 701 EAST TOWER, 555 13TH ST., N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/474,420
;      FILING DATE:  7-JUNE-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/154,712
;      FILING DATE:  19-NOV-1993
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;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/841,961
;      FILING DATE:  26-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/662,222
;      FILING DATE:  22-FEB-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/574,994
;      FILING DATE:  29-AUG-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  UK 8919607.5
;      FILING DATE:  30-AUG-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  NEWLAND, BART
;      REFERENCE/DOCKET NUMBER:  1808-188A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-783-6040
;      TELEFAX:  202-783-6031
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11288 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  N-terminal
US-08-474-420-4

  Query Match             99.8%;  Score 471;  DB 9;  Length 11288;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-113;
  Matches  471;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10294 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 10353

Qy         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10354 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 10413

Qy        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10414 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 10473

Qy        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10474 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 10533

Qy        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10534 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 10593

Qy        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10594 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 10653

Qy        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10654 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 10713

Qy        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10714 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 10764


RESULT 13
US-08-547-142-4
; Sequence 4, Application US/08547142
;  GENERAL INFORMATION:
;    APPLICANT:  HUBER, BRIAN
;    APPLICANT:  RICHARDS, CYNTHIA A
;    APPLICANT:  AUSTIN, ELIZABETH A
;    TITLE OF INVENTION:  NOVEL ENTITIES FOR CANCER THERAPY
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ROTHWELL, FIGG, ERNST & KURZ, P.C.
;      STREET:  SUITE 701 EAST TOWER, 555 13TH ST., N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/547,142
;      FILING DATE:  24-OCT-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/154,712
;      FILING DATE:  19-NOV-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/841,961
;      FILING DATE:  26-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/662,222
;      FILING DATE:  22-FEB-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/574,994
;      FILING DATE:  29-AUG-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  UK 8919607.5
;      FILING DATE:  30-AUG-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  NEWLAND, BART
;      REFERENCE/DOCKET NUMBER:  1808-190A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-783-6040
;      TELEFAX:  202-783-6031
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11288 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  N-terminal
US-08-547-142-4

  Query Match             99.8%;  Score 471;  DB 10;  Length 11288;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-113;
  Matches  471;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10294 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 10353

Qy         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10354 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 10413

Qy        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10414 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 10473

Qy        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10474 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 10533

Qy        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300
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Db      10534 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 10593

Qy        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10594 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 10653

Qy        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10654 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 10713

Qy        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 471
                |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10714 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 10764


RESULT 14
US-09-822-634-1
; Sequence 1, Application US/09822634
; GENERAL INFORMATION:
;  APPLICANT: Vile, Richard G.
;  APPLICANT:  Harrington, Kevin
;  APPLICANT:  Bateman, Andrew
;  APPLICANT:  Murphy, Steven
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TISSUE
;  TITLE OF INVENTION:  SPECIFIC GENE REGULATION THERAPY
;  FILE REFERENCE: 07039-289001
;  CURRENT APPLICATION NUMBER: US/09/822,634
;  CURRENT FILING DATE:  2001-03-30
;  PRIOR APPLICATION NUMBER: 60/193,977
;  PRIOR FILING DATE: 2000-03-31
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 11288
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (10804)...(10935)
US-09-822-634-1

  Query Match             99.8%;  Score 471;  DB 34;  Length 11288;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-113;
  Matches  471;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10294 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 10353

Qy         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
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Db      10354 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 10413

Qy        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10414 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 10473

Qy        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10474 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 10533

Qy        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10534 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 10593

Qy        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10594 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 10653

Qy        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
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Db      10654 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 10713

Qy        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 471
                |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10714 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 10764


RESULT 15
US-09-033-555A-25
; Sequence 25, Application US/09033555A
;   GENERAL INFORMATION:
;        APPLICANT: Lamparski, Henry
;                   Schuur, Eric
;                   Henderson, Daniel
;        TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC FOR CELLS
;                            EXPRESSING CARCINOEMBRYONIC ANTIGENS AND METHODS OF USE
;                            THEREOF
;        NUMBER OF SEQUENCES: 25
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: MORRISON & FOERSTER
;             STREET: 755 PAGE MILL ROAD
;             CITY: PALO ALTO
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 94304-1018
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/033,555A
;             FILING DATE: 02-Mar-1998
;             CLASSIFICATION: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: POLIZZI, CATHERINE M.
;             REGISTRATION NUMBER: 40,130
;             REFERENCE/DOCKET NUMBER: 34802-30005.00
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 813-5600
;             TELEFAX: (415) 494-0792
;             TELEX: 706141 MRSNFOERS SFO
;   INFORMATION FOR SEQ ID NO: 25:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 15056 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-033-555A-25

  Query Match             99.8%;  Score 471;  DB 15;  Length 15056;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-113;
  Matches  471;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14062 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 14121

Qy         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14122 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 14181

Qy        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14182 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 14241

Qy        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14242 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 14301

Qy        241 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14302 GCCGAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGA 14361
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Qy        301 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14362 GGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCATGACCCA 14421

Qy        361 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14422 CGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACA 14481

Qy        421 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14482 GCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 14532
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Search completed: December 11, 2004, 09:53:13
Job time : 3799 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 11, 2004, 06:59:48 ; Search time 158 Seconds
(without alignments)
4578.586 Million cell updates/sec

Title: US-10-045-116-1
Perfect score: 472
Sequence: 1 AGCCACCACCCAGTGAGCCT.....ACGTTCCTGGAACTCAAGCA 472

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1633475 seqs, 766331085 residues

Total number of hits satisfying chosen parameters: 3266950

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_New:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	263.2	55.8	15862	6	US-10-737-082-14	Sequence 14, Appl
	2	103.2	21.9	22140	6	US-10-737-082-68	Sequence 68, Appl
	3	75	15.9	2799	6	US-10-912-745A-360	Sequence 360, App
	4	75	15.9	2799	8	US-60-625-561-294	Sequence 294, App
	5	75	15.9	2799	8	US-60-625-562-301	Sequence 301, App
	6	75	15.9	2974	6	US-10-482-029-240	Sequence 240, App
	7	75	15.9	2974	8	US-60-625-561-293	Sequence 293, App
	8	75	15.9	2974	8	US-60-625-562-300	Sequence 300, App
	9	75	15.9	2976	6	US-10-912-745A-361	Sequence 361, App
	10	75	15.9	2976	8	US-60-625-561-292	Sequence 292, App
	11	75	15.9	2976	8	US-60-625-562-299	Sequence 299, App
c	12	55.4	11.7	294	6	US-10-961-527-311	Sequence 311, App
	13	43.2	9.2	366	6	US-10-948-737-3964	Sequence 3964, Ap
	14	43.2	9.2	472	6	US-10-948-737-3813	Sequence 3813, Ap
c	15	39.4	8.3	54574	6	US-10-990-328-95976	Sequence 95976, A
	16	38	8.1	299	6	US-10-220-366A-11800	Sequence 11800, A
c	17	37.6	8.0	312644	6	US-10-990-328-96981	Sequence 96981, A
c	18	37.4	7.9	13277	6	US-10-990-328-96790	Sequence 96790, A
c	19	37.4	7.9	69757	6	US-10-990-328-94219	Sequence 94219, A
	20	37.2	7.9	98532	6	US-10-990-328-95593	Sequence 95593, A
	21	37	7.8	432	6	US-10-220-366A-12791	Sequence 12791, A
c	22	37	7.8	574	6	US-10-863-332-33	Sequence 33, Appl
c	23	36.6	7.8	206746	6	US-10-990-328-97314	Sequence 97314, A
c	24	36.2	7.7	1285	6	US-10-220-366A-6728	Sequence 6728, Ap
	25	36.2	7.7	9535	6	US-10-912-745A-371	Sequence 371, App
	26	36.2	7.7	15534	6	US-10-956-157-2535	Sequence 2535, Ap
	27	36.2	7.7	15534	6	US-10-912-745A-372	Sequence 372, App
c	28	36.2	7.7	108432	6	US-10-990-328-96484	Sequence 96484, A
	29	36	7.6	67982	6	US-10-990-328-95731	Sequence 95731, A
	30	36	7.6	93741	6	US-10-990-328-93665	Sequence 93665, A
	31	35.8	7.6	600	1	PCT-US04-35274-16040	Sequence 16040, A
	32	35.8	7.6	600	1	PCT-US04-35274-16041	Sequence 16041, A
	33	35.8	7.6	600	1	PCT-US04-35274-16042	Sequence 16042, A
	34	35.8	7.6	600	1	PCT-US04-35274-16043	Sequence 16043, A
	35	35.8	7.6	600	1	PCT-US04-35274-16044	Sequence 16044, A
c	36	35.8	7.6	34406	6	US-10-990-328-93296	Sequence 93296, A
	37	35.8	7.6	232641	6	US-10-990-328-93650	Sequence 93650, A
	38	35.4	7.5	201	6	US-10-990-328-354046	Sequence 354046,
	39	35.4	7.5	201	6	US-10-990-328-354047	Sequence 354047,
	40	35.4	7.5	201	6	US-10-990-328-354048	Sequence 354048,
	41	35.4	7.5	201	6	US-10-990-328-354049	Sequence 354049,
	42	35.4	7.5	201	6	US-10-990-328-354057	Sequence 354057,
	43	35.4	7.5	246385	6	US-10-990-328-95576	Sequence 95576, A
	44	35.2	7.5	201	6	US-10-995-561-50506	Sequence 50506, A
	45	35.2	7.5	148764	6	US-10-990-328-93578	Sequence 93578, A

ALIGNMENTS

RESULT 1
US-10-737-082-14
; Sequence 14, Application US/10737082
; GENERAL INFORMATION:
; APPLICANT: Bayer Healthcare LLC
; APPLICANT: Beard, Chris
; APPLICANT: Burgess, Chris
; APPLICANT: Gannon, Allison
; APPLICANT: Harvey, Jeanne
; APPLICANT: Lechner, John F.
; APPLICANT: Li, Zheng
; TITLE OF INVENTION: Identification and Verification of Methylation Marker Sequences
; FILE REFERENCE: 1657/2032
; CURRENT APPLICATION NUMBER: US/10/737,082
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: US 10/737,082
; PRIOR FILING DATE: 2003-12-16
; NUMBER OF SEQ ID NOS: 300
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 15862
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-737-082-14

Query Match 55.8%; Score 263.2; DB 6; Length 15862;
Best Local Similarity 80.1%; Pred. No. 1.3e-63;
Matches 383; Conservative 0; Mismatches 63; Indels 32; Gaps 5;

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Qy          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
              || || | ||||||||||| |||||| ||||||||||||||||||||||||||||||| ||
Db        515 AGTCATCCCCCAGTGAGCCCCTTTCTATCCCCCAGAGCCACCTCTGTCACCTTCCTGCTG 574

Qy         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
              |||||||||||| |                          || |||| | ||| ||||||
Db        575 GGCATCATCCCAGCA----------------------GAAACCCAAGGCCCAGCTGGG 610

Qy        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAG 180
              |||||||||||| |||| ||||||||||||||||||||||||||||| ||||||||||
Db        611 TTTCTCTGTCAC-AAGGGAAATAATCCCCCTGGTGTGACAGACCCAAGGCCAGAACACAG 669

Qy        181 CAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTT 240
              || |||||||||||||| ||| |||||||||||||||| |||||||||| ||||
Db        670 CATAGGTCAGCACTGGGAAAGGTTGGTTGTCCTCCCAGGGGACAGGGGTCCATCAGCCTT 729

Qy        241 GC--CGAAAAGATTTGTCTGAGGAACTGAAAATAG----AAGGGAAAAAAGAGGAGGGAC 294
              ||  |  |||| ||||| |  |||||||| ||||    |||||||| | || |||||||
Db        730 GCTACTCAAAGCTTTGTATCGGGAACTGAATATAGACAAAAGGGAAAGAGGAAGAGGGAC 789
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Qy        295 AAAAGAGGCAGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGACCACACCCAT 354
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Db        790 AAAAGAGGCAGGAATGAGAGGGGAGGGGACAGAGGACTCCTGAGCAGAGACCCCACCCCT 849

Qy        355 GACCCACGTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGA 414
              |  ||| |||||  ||  |||| |||||||||| ||| ||| |||||  |||||| ||||
Db        850 GGACCATGTGATCTTGGAAAGTGCTCCTGCCCTGGGAGGAGGCTCAGCACAGAGGTAGGA 909

Qy        415 AGGACAGCAGACCAGACAGTCACAGCAGCCTTGACAA-AACGTTCCTGGAACTCAAGC 471
              |||||||||||| | ||||||||||||||| |||||| |  ||||||||| | |||||
Db        910 AGGACAGCAGAGCTGACAGTCACAGCAGCCCTGACAAGAGAGTTCCTGGAGCCCAAGC 967


RESULT 2
US-10-737-082-68
; Sequence 68, Application US/10737082
; GENERAL INFORMATION:
;  APPLICANT: Bayer Healthcare LLC
;  APPLICANT:  Beard, Chris
;  APPLICANT:  Burgess, Chris
;  APPLICANT:  Gannon, Allison
;  APPLICANT:  Harvey, Jeanne
;  APPLICANT:  Lechner, John F.
;  APPLICANT:  Li, Zheng
;  TITLE OF INVENTION: Identification and Verification of Methylation Marker Sequences
;  FILE REFERENCE: 1657/2032
;  CURRENT APPLICATION NUMBER: US/10/737,082
;  CURRENT FILING DATE:  2003-12-16
;  PRIOR APPLICATION NUMBER: US 10/737,082
;  PRIOR FILING DATE: 2003-12-16
;  NUMBER OF SEQ ID NOS: 300
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 68
;   LENGTH: 22140
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-737-082-68

  Query Match             21.9%;  Score 103.2;  DB 6;  Length 22140;
  Best Local Similarity   61.0%;  Pred. No. 1.1e-18;
  Matches  305;  Conservative    0;  Mismatches  158;  Indels   37;  Gaps    7;

Qy          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
              || || | |||||||||||   |||| | ||||||||||||||||||||||||||||| ||
Db        542 AGTCATCCCCCAGTGAGCCCCTTTCCATCCCCCAGAGCCACCTCTGTCACCTTCCTGCTG 601

Qy         61 GGCATCATCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
              ||  || ||| ||||||||||   | ||| ||||||||||||||| || | |   ||| |
Db        602 GGTGTCTTCCTACCTTCCCAGCACACTGAAGAGCATGGGGAGACCTGGCAGCTCACTGTG 661

Qy        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGG-------------------TGTGACAG 161
              || |   |  |  ||  |  | | |       |                   ||||||
Db        662 TTGCAAAGAAAATAATTACCACATTTGGATATGCCAGGGTTCTCTGTGTGCTGCTGACAG 721

Qy        162 ACCCAAGGACAGAACACAGCAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCC----- 216
              |||||  | ||| |||||  |||||||||  |||| || |   | |  |||||||
Db        722 ACCCATAGCCAGGACACAATAGAGGTCAGTGCTGGAGAGGGGGGATCCTCCTCCCCTGAT 781

Qy        217 AGGGGATGGGGGTCCATCCACCTTG--CCGAAAAGATTTGTCTGAGGAACTGAAAATAGA 274
               |||   | ||   ||||  |||||    |  ||||  | ||||| | |||  |||
Db        782 GGGGACAGAGGTCTCATCAGCCTTGATTCTCAAAGTGTGGTCTGGGAAACCAAAATGTAG 841

Qy        275 AGGGAAAAAAGAG---GAGGGACAAAAGAGGCAGAAATGAGAGGGGAGGGGACAGAGGAC 331
              |  ||||  | ||    ||  |  | | ||| || ||||||||| ||||  ||||||
Db        842 ACAGAAAGGAAAGAGAAAGTAAGGACAAAGGTAGGAATGAGAGGAGAGGAAACAGAGCTT 901

Qy        332 ACCTGAATAAAGACCACACCCATGACCCACGTGATGCTGAGAAGTACTCCTGCCCTAGGA 391
              |  ||  ||    | |  ||    | ||| ||||      |||  ||    |||  |||
Db        902 CCTGGACAAA----CCCCGCCCCAGCACACATGATCAGACAAAGCTCTGGGCCCCAGGGA 957

Qy        392 AGAGACTCAGGGCAGAGGGAGGAAGGACAGCAGACCAGACAGTCACAGCAGCCTTGACAA 451
              ||| |||||  ||||| | ||||  ||||||||   |||||      |   ||   | |
Db        958 GGAGGCTCAGCACAGAGAGTGGAA-AACAGCAGAGGTGACAGAGCAGCCGTGCT---CGA 1013

Qy        452 AACGTTCCTGGAACTCAAGC 471
              | |||||||||| | |||||
Db       1014 AGCGTTCCTGGAGCCCAAGC 1033


RESULT 3
US-10-912-745A-360
; Sequence 360, Application US/10912745A
; GENERAL INFORMATION:
;  APPLICANT: Applera Corporation
;  APPLICANT:  DOMON, Bruno et al.
;  TITLE OF INVENTION: Pancreatic Cancer Targets and Uses
;  TITLE OF INVENTION:  Thereof
;  FILE REFERENCE: CL001538
;  CURRENT APPLICATION NUMBER: US/10/912,745A
;  CURRENT FILING DATE:  2004-08-06
;  NUMBER OF SEQ ID NOS: 873
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 360
;   LENGTH: 2799
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-912-745A-360

  Query Match             15.9%;  Score 75;  DB 6;  Length 2799;
  Best Local Similarity   100.0%;  Pred. No. 4.5e-11;
  Matches   75;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        397 CTCAGGGCAGAGGGAGGAAGGACAGCAGACCAGACAGTCACAGCAGCCTTGACAAAACGT 456
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CTCAGGGCAGAGGGAGGAAGGACAGCAGACCAGACAGTCACAGCAGCCTTGACAAAACGT 60

Qy        457 TCCTGGAACTCAAGC 471
              |||||||||||||||
Db         61 TCCTGGAACTCAAGC 75


RESULT 4
US-60-625-561-294
; Sequence 294, Application US/60625561
; GENERAL INFORMATION:
;  APPLICANT: MCCAFFREY, Ian
;  APPLICANT:  DOMON, Bruno
;  TITLE OF INVENTION: PANCREATIC CANCER TARGETS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL001557
;  CURRENT APPLICATION NUMBER: US/60/625,561
;  CURRENT FILING DATE:  2004-11-08
;  NUMBER OF SEQ ID NOS: 586
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 294
;   LENGTH: 2799
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-60-625-561-294

  Query Match             15.9%;  Score 75;  DB 8;  Length 2799;
  Best Local Similarity   100.0%;  Pred. No. 4.5e-11;
  Matches   75;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        397 CTCAGGGCAGAGGGAGGAAGGACAGCAGACCAGACAGTCACAGCAGCCTTGACAAAACGT 456
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CTCAGGGCAGAGGGAGGAAGGACAGCAGACCAGACAGTCACAGCAGCCTTGACAAAACGT 60

Qy        457 TCCTGGAACTCAAGC 471
              |||||||||||||||
Db         61 TCCTGGAACTCAAGC 75


RESULT 5
US-60-625-562-301
```

```
; Sequence 301, Application US/60625562
; GENERAL INFORMATION:
;  APPLICANT: MCCAFFREY, Ian
;  APPLICANT:  DOMON, Bruno
;  TITLE OF INVENTION: COLON DISEASE TARGETS AND USES THEREOF
;  FILE REFERENCE: CL001555
;  CURRENT APPLICATION NUMBER: US/60/625,562
;  CURRENT FILING DATE:  2004-11-08
;  NUMBER OF SEQ ID NOS: 535
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 301
;   LENGTH: 2799
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-60-625-562-301

  Query Match             15.9%;  Score 75;  DB 8;  Length 2799;
  Best Local Similarity   100.0%;  Pred. No. 4.5e-11;
  Matches   75;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        397 CTCAGGGCAGAGGGAGGAAGGACAGCAGACCAGACAGTCACAGCAGCCTTGACAAAACGT 456
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CTCAGGGCAGAGGGAGGAAGGACAGCAGACCAGACAGTCACAGCAGCCTTGACAAAACGT 60

Qy        457 TCCTGGAACTCAAGC 471
              |||||||||||||||
Db         61 TCCTGGAACTCAAGC 75


RESULT 6
US-10-482-029-240
; Sequence 240, Application US/10482029
; GENERAL INFORMATION:
;  APPLICANT: ODIN medical A/S
;  TITLE OF INVENTION: Oncology drug innovation
;  FILE REFERENCE: P 573 PC00
;  CURRENT APPLICATION NUMBER: US/10/482,029
;  CURRENT FILING DATE:  2003-12-29
;  NUMBER OF SEQ ID NOS: 437
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 240
;   LENGTH: 2974
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-482-029-240

  Query Match             15.9%;  Score 75;  DB 6;  Length 2974;
  Best Local Similarity   100.0%;  Pred. No. 4.5e-11;
  Matches   75;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        397 CTCAGGGCAGAGGGAGGAAGGACAGCAGACCAGACAGTCACAGCAGCCTTGACAAAACGT 456
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CTCAGGGCAGAGGGAGGAAGGACAGCAGACCAGACAGTCACAGCAGCCTTGACAAAACGT 60

Qy        457 TCCTGGAACTCAAGC 471
              |||||||||||||||
Db         61 TCCTGGAACTCAAGC 75


RESULT 7
US-60-625-561-293
; Sequence 293, Application US/60625561
; GENERAL INFORMATION:
;  APPLICANT: MCCAFFREY, Ian
;  APPLICANT:  DOMON, Bruno
;  TITLE OF INVENTION: PANCREATIC CANCER TARGETS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL001557
;  CURRENT APPLICATION NUMBER: US/60/625,561
;  CURRENT FILING DATE:  2004-11-08
;  NUMBER OF SEQ ID NOS: 586
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 293
;   LENGTH: 2974
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-60-625-561-293

  Query Match             15.9%;  Score 75;  DB 8;  Length 2974;
  Best Local Similarity   100.0%;  Pred. No. 4.5e-11;
  Matches   75;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        397 CTCAGGGCAGAGGGAGGAAGGACAGCAGACCAGACAGTCACAGCAGCCTTGACAAAACGT 456
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CTCAGGGCAGAGGGAGGAAGGACAGCAGACCAGACAGTCACAGCAGCCTTGACAAAACGT 60

Qy        457 TCCTGGAACTCAAGC 471
              |||||||||||||||
Db         61 TCCTGGAACTCAAGC 75


RESULT 8
US-60-625-562-300
; Sequence 300, Application US/60625562
; GENERAL INFORMATION:
;  APPLICANT: MCCAFFREY, Ian
;  APPLICANT:  DOMON, Bruno
;  TITLE OF INVENTION: COLON DISEASE TARGETS AND USES THEREOF
;  FILE REFERENCE: CL001555
;  CURRENT APPLICATION NUMBER: US/60/625,562
;  CURRENT FILING DATE:  2004-11-08
;  NUMBER OF SEQ ID NOS: 535
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 300
;   LENGTH: 2974
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-60-625-562-300

  Query Match             15.9%;  Score 75;  DB 8;  Length 2974;
  Best Local Similarity   100.0%;  Pred. No. 4.5e-11;
  Matches   75;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        397 CTCAGGGCAGAGGGAGGAAGGACAGCAGACCAGACAGTCACAGCAGCCTTGACAAAACGT 456
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CTCAGGGCAGAGGGAGGAAGGACAGCAGACCAGACAGTCACAGCAGCCTTGACAAAACGT 60

Qy        457 TCCTGGAACTCAAGC 471
              |||||||||||||||
Db         61 TCCTGGAACTCAAGC 75


RESULT 9
US-10-912-745A-361
; Sequence 361, Application US/10912745A
; GENERAL INFORMATION:
;  APPLICANT: Applera Corporation
;  APPLICANT:  DOMON, Bruno et al.
;  TITLE OF INVENTION: Pancreatic Cancer Targets and Uses
;  TITLE OF INVENTION:  Thereof
;  FILE REFERENCE: CL001538
;  CURRENT APPLICATION NUMBER: US/10/912,745A
;  CURRENT FILING DATE:  2004-08-06
;  NUMBER OF SEQ ID NOS: 873
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 361
;   LENGTH: 2976
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-912-745A-361

  Query Match             15.9%;  Score 75;  DB 6;  Length 2976;
  Best Local Similarity   100.0%;  Pred. No. 4.5e-11;
  Matches   75;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        397 CTCAGGGCAGAGGGAGGAAGGACAGCAGACCAGACAGTCACAGCAGCCTTGACAAAACGT 456
```

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CTCAGGGCAGAGGGAGGAAGGACAGCAGACCAGACAGTCACAGCAGCCTTGACAAAACGT 60

Qy        457 TCCTGGAACTCAAGC 471
              |||||||||||||||
Db         61 TCCTGGAACTCAAGC 75


RESULT 10
US-60-625-561-292
; Sequence 292, Application US/60625561
; GENERAL INFORMATION:
;  APPLICANT: MCCAFFREY, Ian
;  APPLICANT:  DOMON, Bruno
;  TITLE OF INVENTION: PANCREATIC CANCER TARGETS AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL001557
;  CURRENT APPLICATION NUMBER: US/60/625,561
;  CURRENT FILING DATE:  2004-11-08
;  NUMBER OF SEQ ID NOS: 586
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 292
;   LENGTH: 2976
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-60-625-561-292

  Query Match             15.9%;  Score 75;  DB 8;  Length 2976;
  Best Local Similarity   100.0%;  Pred. No. 4.5e-11;
  Matches   75;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        397 CTCAGGGCAGAGGGAGGAAGGACAGCAGACCAGACAGTCACAGCAGCCTTGACAAAACGT 456
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CTCAGGGCAGAGGGAGGAAGGACAGCAGACCAGACAGTCACAGCAGCCTTGACAAAACGT 60

Qy        457 TCCTGGAACTCAAGC 471
              |||||||||||||||
Db         61 TCCTGGAACTCAAGC 75


RESULT 11
US-60-625-562-299
; Sequence 299, Application US/60625562
; GENERAL INFORMATION:
;  APPLICANT: MCCAFFREY, Ian
;  APPLICANT:  DOMON, Bruno
;  TITLE OF INVENTION: COLON DISEASE TARGETS AND USES THEREOF
;  FILE REFERENCE: CL001555
;  CURRENT APPLICATION NUMBER: US/60/625,562
;  CURRENT FILING DATE:  2004-11-08
;  NUMBER OF SEQ ID NOS: 535
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 299
;   LENGTH: 2976
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-60-625-562-299

  Query Match             15.9%;  Score 75;  DB 8;  Length 2976;
  Best Local Similarity   100.0%;  Pred. No. 4.5e-11;
  Matches   75;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        397 CTCAGGGCAGAGGGAGGAAGGACAGCAGACCAGACAGTCACAGCAGCCTTGACAAAACGT 456
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CTCAGGGCAGAGGGAGGAAGGACAGCAGACCAGACAGTCACAGCAGCCTTGACAAAACGT 60

Qy        457 TCCTGGAACTCAAGC 471
              |||||||||||||||
Db         61 TCCTGGAACTCAAGC 75


RESULT 12
US-10-961-527-311/c
; Sequence 311, Application US/10961527
; GENERAL INFORMATION:
;  APPLICANT: King, Gordon E.
;  APPLICANT:  Meagher, Madeleine Joy
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Secrist, Heather
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF COLON CANCER
;  FILE REFERENCE: 210121.547C4
;  CURRENT APPLICATION NUMBER: US/10/961,527
;  CURRENT FILING DATE:  2004-10-07
;  PRIOR APPLICATION NUMBER: US 09/920,300
;  PRIOR FILING DATE: 2001-07-31
;  PRIOR APPLICATION NUMBER: US 60/302,051
;  PRIOR FILING DATE: 2001-06-29
;  PRIOR APPLICATION NUMBER: US 60/279,763
;  PRIOR FILING DATE: 2001-03-28
;  PRIOR APPLICATION NUMBER: US 60/223,283
;  PRIOR FILING DATE: 2000-08-03
;  NUMBER OF SEQ ID NOS: 1789
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 311
;   LENGTH: 294
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-961-527-311

  Query Match             11.7%;  Score 55.4;  DB 6;  Length 294;
  Best Local Similarity   98.2%;  Pred. No. 6.5e-06;
  Matches   56;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        415 AGGACAGCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 471
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        293 ACGACAGCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAACTCAAGC 237


RESULT 13
US-10-948-737-3964
; Sequence 3964, Application US/10948737
; GENERAL INFORMATION:
;  APPLICANT: CHAN, VIVIEN W.
;  APPLICANT:  ESCOBEDO, JAIME
;  APPLICANT:  GARCIA, PABLO DOMINGUEZ
;  APPLICANT:  HANSEN, RHONDA
;  APPLICANT:  KAUFMANN, JOERG
;  APPLICANT:  KENNEDY, GIULIA C.
;  APPLICANT:  LAMSON, GEORGE
;  APPLICANT:  MOLER, EDWARD J.
;  APPLICANT:  RANDAZZO, FILIPPO
;  APPLICANT:  REINHARD, CHRISTOPH
;  APPLICANT:  SUDDUTH-KLINGER, JULIE
;  TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED
;  TITLE OF INVENTION:  IN CANCEROUS CELLS III
;  FILE REFERENCE: 2300-21987
;  CURRENT APPLICATION NUMBER: US/10/948,737
;  CURRENT FILING DATE:  2004-09-22
;  PRIOR APPLICATION NUMBER: 10/616,900
;  PRIOR FILING DATE: 2003-07-09
;  PRIOR APPLICATION NUMBER: 09/872,850
;  PRIOR FILING DATE: 2001-06-01
;  PRIOR APPLICATION NUMBER: 60/208,871
;  PRIOR FILING DATE: 2000-06-02
;  PRIOR APPLICATION NUMBER: 10/081,519
;  PRIOR FILING DATE: 2002-02-21
;  PRIOR APPLICATION NUMBER: 60/270,959
;  PRIOR FILING DATE: 2001-02-21
;  PRIOR APPLICATION NUMBER: 10/310,673
;  PRIOR FILING DATE: 2003-01-08
;  PRIOR APPLICATION NUMBER: 60/336,613
;  PRIOR FILING DATE: 2001-12-04
;  PRIOR APPLICATION NUMBER: US03/00657
;  PRIOR FILING DATE: 2003-01-08
;  PRIOR APPLICATION NUMBER: 60/345,637
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;  PRIOR FILING DATE: 2002-01-08
;  PRIOR APPLICATION NUMBER: 10/081,124
;  PRIOR FILING DATE: 2002-02-21
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 13996
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3964
;   LENGTH: 366
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-948-737-3964

  Query Match             9.2%;  Score 43.2;  DB 6;  Length 366;
  Best Local Similarity   86.8%;  Pred. No. 0.018;
  Matches   59;  Conservative    0;  Mismatches    8;  Indels    1;  Gaps    1;

Qy        405 AGAGGGAGGAAGGACAGCAGACCAGACAGTCACAGCAGCCTTGACAAAAC-GTTCCTGGA 463
              ||||| |||||||||||||||| | |||||||||||||||| |||||| |  |||||||||
Db          2 AGAGGTAGGAAGGACAGCAGAGCTGACAGTCACAGCAGCCCTGACAAGAGAGTTCCTGGA 61

Qy        464 ACTCAAGC 471
              | |||||
Db         62 GCCCAAGC 69


RESULT 14
US-10-948-737-3813
; Sequence 3813, Application US/10948737
; GENERAL INFORMATION:
;  APPLICANT: CHAN, VIVIEN W.
;  APPLICANT:  ESCOBEDO, JAIME
;  APPLICANT:  GARCIA, PABLO DOMINGUEZ
;  APPLICANT:  HANSEN, RHONDA
;  APPLICANT:  KAUFMANN, JOERG
;  APPLICANT:  KENNEDY, GIULIA C.
;  APPLICANT:  LAMSON, GEORGE
;  APPLICANT:  MOLER, EDWARD J.
;  APPLICANT:  RANDAZZO, FILIPPO
;  APPLICANT:  REINHARD, CHRISTOPH
;  APPLICANT:  SUDDUTH-KLINGER, JULIE
;  TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED
;  TITLE OF INVENTION:  IN CANCEROUS CELLS III
;  FILE REFERENCE: 2300-21987
;  CURRENT APPLICATION NUMBER: US/10/948,737
;  CURRENT FILING DATE:  2004-09-22
;  PRIOR APPLICATION NUMBER: 10/616,900
;  PRIOR FILING DATE: 2003-07-09
;  PRIOR APPLICATION NUMBER: 09/872,850
;  PRIOR FILING DATE: 2001-06-01
;  PRIOR APPLICATION NUMBER: 60/208,871
;  PRIOR FILING DATE: 2000-06-02
;  PRIOR APPLICATION NUMBER: 10/081,519
;  PRIOR FILING DATE: 2002-02-21
;  PRIOR APPLICATION NUMBER: 60/270,959
;  PRIOR FILING DATE: 2001-02-21
;  PRIOR APPLICATION NUMBER: 10/310,673
;  PRIOR FILING DATE: 2003-01-08
;  PRIOR APPLICATION NUMBER: 60/336,613
;  PRIOR FILING DATE: 2001-12-04
;  PRIOR APPLICATION NUMBER: US03/00657
;  PRIOR FILING DATE: 2003-01-08
;  PRIOR APPLICATION NUMBER: 60/345,637
;  PRIOR FILING DATE: 2002-01-08
;  PRIOR APPLICATION NUMBER: 10/081,124
;  PRIOR FILING DATE: 2002-02-21
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 13996
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3813
;   LENGTH: 472
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-948-737-3813

  Query Match             9.2%;  Score 43.2;  DB 6;  Length 472;
  Best Local Similarity   86.8%;  Pred. No. 0.02;
  Matches   59;  Conservative    0;  Mismatches    8;  Indels    1;  Gaps    1;

Qy        405 AGAGGGAGGAAGGACAGCAGACCAGACAGTCACAGCAGCCTTGACAAAAC-GTTCCTGGA 463
              ||||| |||||||||||||||| | |||||||||||||||| |||||| |  |||||||||
Db          1 AGAGGTAGGAAGGACAGCAGAGCTGACAGTCACAGCAGCCCTGACAAGAGAGTTCCTGGA 60

Qy        464 ACTCAAGC 471
              | |||||
Db         61 GCCCAAGC 68


RESULT 15
US-10-990-328-95976/c
; Sequence 95976, Application US/10990328
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele
;  TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
;  TITLE OF INVENTION:  ENCODING HUMAN ENZYME PROTEINS, METHODS OF DETECTION AND
;  TITLE OF INVENTION:  USES THEREOF
;  FILE REFERENCE: CL001495
;  CURRENT APPLICATION NUMBER: US/10/990,328
;  CURRENT FILING DATE:  2004-11-17
;  NUMBER OF SEQ ID NOS: 558824
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 95976
;   LENGTH: 54574
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-990-328-95976

  Query Match             8.3%;  Score 39.4;  DB 6;  Length 54574;
  Best Local Similarity   51.6%;  Pred. No. 1.2;
  Matches  114;  Conservative    0;  Mismatches  106;  Indels    1;  Gaps    1;

Qy        124 CTCTGTCACAAAGGAAAATAATCCCCCTGGTGTGACAGACCCAAGGACAGAACACAGCAG 183
              || || | || ||||| ||      || | ||  | ||   | ||   || || |||||
Db       8846 CTGTGACCCACAGGAAGATGGAAACCGTTGTAAGCCATGTCTAAAAGCA-AAAACAGCTC 8788

Qy        184 AGGTCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTTGCC 243
              | |      | | ||||  |    |  | ||  ||||   || ||       |
Db       8787 AAGGTGTTTCAGAGGAAAGCTCTCTACCTTCAGAGGGAGGGGAGGAGAGGGGAGAAAAGG 8728

Qy        244 GAAAAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGAGGC 303
              | || |    |  |||||    || ||  | ||  ||| | |||||||   | ||   |
Db       8727 GGAATGGAGGGGGTGAGGGGAGGAGAAGTGGAGAAAAAGAGGAGGAGGAGAAGAAAGAGG 8668

Qy        304 AGAAATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGA 344
              || |   || | | ||||||  |||||  |   ||  |||||
Db       8667 AGGAGGAAGGGAGAAGGGGAAGGAGGAGAAAGGATGAAAGA 8627


Search completed: December 11, 2004, 09:55:58
Job time : 160 secs
```

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 11, 2004, 06:27:49 ; Search time 2957 Seconds
(without alignments)
5816.555 Million cell updates/sec

Title: US-10-045-116-1
Perfect score: 472
Sequence: 1 AGCCACCACCCAGTGAGCCT.....ACGTTCCTGGAACTCAAGCA 472

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	87.8	18.6	328	2	AW449279	UI-H-BI3-
2	78.4	16.6	701	9	AG307251	AG307251 Mus muscu
3	75.2	15.9	522	8	AZ553789	AZ553789 RPCI-23-1
4	71	15.0	588	8	AZ377232	AZ377232 1M0131P23
5	71	15.0	594	6	CD709204	CD709204 EST25731
6	69.8	14.8	177	6	CD708401	CD708401 EST24928
7	69.8	14.8	338	6	CD685182	CD685182 EST1702 h
8	69.8	14.8	555	6	CD691155	CD691155 EST7678 h
9	69	14.6	595	1	AL602851	AL602851 DKFZp686P
10	68.8	14.6	787	1	AU140869	AU140869
11	67.6	14.3	552	6	CD686649	CD686649 EST3170 h
12	67	14.2	220	4	BM829043	BM829043 K-EST0101
13	67	14.2	275	4	BM836430	BM836430 K-EST0112
14	67	14.2	279	4	BM752482	BM752482 K-EST0029
15	67	14.2	355	4	BM836104	BM836104 K-EST0111
16	67	14.2	418	4	BM751932	BM751932 K-EST0028
17	67	14.2	483	4	BM828560	BM828560 K-EST0101
18	67	14.2	569	4	BM836866	BM836866 K-EST0112
19	65.4	13.9	310	5	BX950909	BX950909 DKFZp781B
20	64.6	13.7	534	4	BM752131	BM752131 K-EST0028
21	63	13.3	879	8	AQ746357	AQ746357 HS_2278_A
22	62.8	13.3	632	9	CE403021	CE403021 tigr-gss-
c 23	62	13.1	195	2	AW839587	AW839587 RC6-LT007
24	62	13.1	490	6	CD618569	CD618569 56076560J
25	61	12.9	651	1	AL602396	AL602396 DKFZp686F
26	60	12.7	716	6	CD618550	CD618550 56043842H
27	60	12.7	729	6	CD618558	CD618558 56044026H
28	60	12.7	803	6	CD618546	CD618546 56043758H
29	60	12.7	841	6	CD618552	CD618552 56043850H
30	59	12.5	390	1	AA132598	AA132598 zo17c08.r
31	59	12.5	489	6	CD618563	CD618563 56076536J
32	59	12.5	579	6	CD618516	CD618516 56019457H
33	59	12.5	670	6	CD618510	CD618510 56019433H
34	58.4	12.4	548	6	CD618545	CD618545 56043734J
35	58.4	12.4	726	6	CD618556	CD618556 56043910H
36	58.4	12.4	823	6	CD618555	CD618555 56043858J
37	57.6	12.2	512	6	CD696697	CD696697 EST13220
38	57.4	12.2	486	6	CD618565	CD618565 56076544J
39	57.4	12.2	574	5	BX479959	BX479959 DKFZp686M
40	57.2	12.1	557	6	CD691034	CD691034 EST7557 h
41	57	12.1	180	6	CD618536	CD618536 56027690H
42	56	11.9	887	4	BI759915	BI759915 603044336
43	55	11.7	380	1	AA132182	AA132182 zo28b09.r
44	54.2	11.5	534	6	CD691079	CD691079 EST7602 h
45	53.4	11.3	677	6	CD618515	CD618515 56019449J

ALIGNMENTS

RESULT 1
AW449279
LOCUS AW449279 328 bp mRNA linear EST 17-FEB-2000
DEFINITION UI-H-BI3-akh-e-09-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734193 3', mRNA sequence.
ACCESSION AW449279
VERSION AW449279.1 GI:6990055
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 328)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward
POLYA=Yes.
FEATURES Location/Qualifiers
source 1. .328
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2734193"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_Sub5"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; NCI_CGAP_Sub5 is a subtracted library derived from NCI_CGAP_Sub4. The NCI_CGAP_Sub5 library had 3 million recombinants. A single-stranded DNA preparation of NCI_CGAP_Sub4 was used as a tracer in a subtractive hybridization with a driver comprising: the IMAGE pool (NCI_CGAP_Kid3 pool 1 LLAM 3334-3337, 3682-3683, 3798-3803 (IMAGE CloneIDs 1322376-1323911, 1456008-1456775,1500552-1502855); NCI_CGAP_Kid5 pool 1 LLAM 3338-3342,3722-3725, 3776-3778 (IMAGE CloneIDs 1323912-1325831, 1471368-1472903,

1492104-1493255); NCI_CGAP_Lu5 pool 1 LLAM 3575-3582, 3851-3854 (IMAGE CloneIDs 1414920-1417991,1520904-1522439); NCI_CGAP_GC4 pool 1 LLAM 3164-3167, 3716-3720, 3733-3735 (IMAGE CloneIDs 1257096-1258631,1469064-1470983, 1475592-1476743); NCI_CGAP_Pr22 pool 1 LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE CloneIDs 985608-986759,1101192-1101959, 1217928-1220615); NCI_CGAP_Co10 pool 1 LLAM 2644-2653, 2871-2872 (IMAGE CloneIDs 1057416-1061255,1144584-1145351). (10% of the driver population), plus a pool of 3,840 arrayed clones from NCI_CGAP_Sub1 (IMAGE CloneIDs 2708616-2710535) and NCI_CGAP_Sub2 (IMAGE CloneIDs 2710536-2712455) (10% of the driver population), plus a pool of 11,136 clones from NCI_CGAP_Sub3 (IMAGE CloneIDs 2712456-2723591) (10% of the driver population), plus a pool of 5,472 clones from NCI_CGAP_Sub4 (IMAGE CloneIDs 2723592-2728969) (70% of the driver population). Subtraction was performed as previously described [Bonaldo, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome Research 6, 791-806. TAG_TISSUE=colon TAG_LIB=NCI_CGAP_Co10 TAG_SEQ=AAACG"

ORIGIN

Query Match 18.6%; Score 87.8; DB 2; Length 328;
Best Local Similarity 65.5%; Pred. No. 6.5e-13;
Matches 154; Conservative 0; Mismatches 62; Indels 19; Gaps 1;

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Qy          1 AGCCACCACCCAGTGAGCCTTTTTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTG 60
              || || | ||||||||||  |||| | ||||||||||||||||||||||||||||||||
Db         35 AGTCATCCCCCAGTGAGCCCCTTTCCATCCCCCAGAGCCACCTCTGTCACCTTCCTGCTG 94

Qy         61 GGCATCATCCCCACCTTCCCAGAGCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGG 120
              ||  || ||| ||||||||||  | ||| ||||||||||||||||| || | |   ||| |
Db         95 GGTGTCTTCCTACCTTCCCAGCACACTGAAGAGCATGGGGAGACCTGGCAGCTCACTGTG 154

Qy        121 TTTCTCTGTCACAAAGGAAAATAATCCCCCTGG------------------TGTGACAG 161
              || |   |  |  ||  |  | | |       |                  ||||||
Db        155 TTGCAAAGAAAATAATTACCACATTTGGATATGCCAGGGTTCTCTGTGTGCTGCTGACAG 214

Qy        162 ACCCAAGGACAGAACACAGCAGAGGTCAGCACTGGGGAAGACAGGTTGTCCTCCC 216
              |||||  | ||| |||||  |||||||||  |||| || |   | |  |||||||
Db        215 ACCCATAGCCAGGACACAATAGAGGTCAGTGCTGGAGAGGGGGGATCCTCCTCCC 269
```

RESULT 2
AG307251
LOCUS AG307251 701 bp DNA linear GSS 02-JUN-2004
DEFINITION Mus musculus molossinus DNA, clone:MSMg01-088I06.TJ, genomic survey sequence.
ACCESSION AG307251
VERSION AG307251.1 GI:47880205
KEYWORDS GSS.
SOURCE Mus musculus molossinus
ORGANISM Mus musculus molossinus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
TITLE BAC end Sequences of Library MSMg01
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 701)
AUTHORS Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp).

Tsukuba Institude, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp
PRIMERS
Sequencing : TJ
LIBRARY
Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI.
FEATURES Location/Qualifiers
source 1. .701
/organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="MSMg01-088I06.TJ"
/sex="male"
/tissue_type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"

ORIGIN

Query Match 16.6%; Score 78.4; DB 9; Length 701;
Best Local Similarity 56.4%; Pred. No. 2.9e-10;
Matches 239; Conservative 0; Mismatches 161; Indels 24; Gaps 4;

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Qy         23 TTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTGGGCATCATCCCCACCTTCCCAGA 82
              ||| |  | ||  | ||||| |||||||||| || |||| |  ||||||||||||||||
Db        173 TTCCAAACTTCACTGGCACCTGTGTCACCTTCTTGCTGGGAA--ATCCCACCTTCCCAGA 230

Qy         83 GCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGGTTTCTCTGTCACAAAGGAAAAT 142
              |  ||| |||    ||| ||||  ||  | |  |||||| | | |||| ||  || | ||
Db        231 GTACTGAAGACACAGGGCAGACTAGGAGCTCATCTGGGTCTATGTGTCTCAGGGGCACAT 290

Qy        143 AATCCCCCTGGTG----------------TGACAGACCCAAGGACAGAACACAGCAGAGG 186
              |       | | |                ||||||| || |  ||| |  |||||||
Db        291 AGGAAAGATAGAGGTTCCCTCTTTGATGCTGACAGACTCATGTCCAGGAGTCAGCAGATA 350

Qy        187 TCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTTGCCGAA 246
              ||||| |  ||    |    |  ||       ||       |    |    || ||
Db        351 TCAGCGCCTGGATGAATCATTGTTCTCTGAGGGCATGTCGATACTTATCAGCTGTGTTGC 410

Qy        247 AAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGAGGCAGA 306
              |  | |   |||   ||||    ||| || ||||   |||| | |   | ||||
Db        411 TCAAGGTTTTGTTGGAGAAGAAACATAAAGAGAGAAAATTTGAGGAAGATGCGGGGCAGC 470

Qy        307 AATGAGAGGGGAGGGGACAGAGGA-----CACCTGAATAAAGACCACACCCATGACCCAC 361
              | |||||| ||| | ||| ||| |         | |   |   |  ||| ||    |||
Db        471 ACTGAGAGTGGAAGTGACTGAGCAGTGTCGTGGTCACAGACCCCACCACACACAGTCCAT 530

Qy        362 GTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACAG 421
              |||| ||| ||||| |||||| | |  ||  | ||||||  |||| |||||||||||||
Db        531 AGGATTCTGGGAAGTGCTCCTG-CTTGAGAGAAAACTCAGCTCAGAAGGAGGAAGGACAG 589

Qy        422 CAGA 425
              ||||
Db        590 CAGA 593
```

RESULT 3
AZ553789
LOCUS AZ553789 522 bp DNA linear GSS 20-NOV-2000
DEFINITION RPCI-23-177H11.TJ RPCI-23 Mus musculus genomic clone RPCI-23-177H11, genomic survey sequence.
ACCESSION AZ553789
VERSION AZ553789.1 GI:11233609
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 522)

```
  AUTHORS   Zhao,S., Nierman,W., Peldblyum,T., Malek,J., Shatsman,S.,
            Akinret,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de
            Jong,P. and Fraser,C.M.
  TITLE     Mouse BAC End Sequences from Library RPCI-23
  JOURNAL   Unpublished (1999)
COMMENT     Other_GSSs: RPCI-23-177H11.TV
            Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Clones are derived from the mouse BAC library RPCI-23. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
            or from Resea ch Genetics (info@resgen.com). BAC end page:
            http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
            Plate: 177  row: H  column: 11
            Seq primer: SP6
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .522
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="RPCI-23-177H11"
                     /sex="Female"
                     /lab_host="DH10B"
                     /clone_lib="RPCI-23"
                     /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
                     EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
                     brain genomic DNA was isolated and partially digested
                     with a combination of EcoRI and EcoRI Methylase.   Size
                     selected DNA was cloned into the pBACe3.6 vector at the
                     EcoRI  sites.  The ligation products were transformed into
                     DH10B  electrocompetent cells (BRL Life Technologies).   "
ORIGIN

  Query Match           15.9%;  Score 75.2;  DB 8;  Length 522;
  Best Local Similarity   55.9%;  Pred. No. 2e-09;
  Matches  237;  Conservative    0;  Mismatches  163;  Indels   24;  Gaps    4;

Qy         23 TTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTGGGCATCATCCCACCTTCCCAGA 82
              |||  |   |   ||   | |||||  ||||||||||||||| ||||  |   ||||||||||||||||
Db         92 TTCCAAACTTCACTGGCACCTGTGTCACCTTCCTGCTGGGAA--ATCCCACCTTCCCAGA 149

Qy         83 GCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGGTTTCTCTGTCACAAAGGAAAAT 142
              |  |||  |||     |||  |      |  | |  ||||||  | |  ||||  ||   |  | ||
Db        150 GTACTGAAGACACAGGGCTGTTTGTGATCTCATCTGGGTCTATGTGTCTCAGGGACACAT 209

Qy        143 AATCCCCCTGGTG----------------TGACAGACCCAAGGACAGAACACAGCAGAGG 186
              |      | | |                ||||||||  ||  |   |||  |   |||||||
Db        210 AGGAAAGATAGAGGTTCCCTCTTTGATGCTGACAGACTCATGTCCAGGAGTCAGCAGATA 269

Qy        187 TCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTTGCCGAA 246
              |||||  |   ||    |    |  ||       ||       |   |    ||  ||
Db        270 TCAGCGCCTGGATGAATCATTGTTCTCTGAGGGCATGTCGATACTTATCATCTGTGTTGC 329

Qy        247 AAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGAGGCAGA 306
                 |  |  |    |||   ||||    |||  ||  ||||   ||||  |  |    |  |||||
Db        330 TCAAGGTTTTGTTGGAGAAGAAACATAAAGAGAGAAAATGTGAGGAAGATTTGGGGCAGC 389

Qy        307 AATGAGAGGGGAGGGGACAGAGGA-----CACCTGAATAAAGACCACACCCATGACCCAC 361
              | |||||| ||| | |||  ||| |          | |    |   |  |||  ||   ||||
Db        390 ACTGAGAGTGGAAGTGACTGAGCAGTGTCGTGGTCACAGACCCCACCACACACAGCCCAT 449

Qy        362 GTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACAG 421
                ||| |||  |||||  ||||||  |||   ||   |  ||||||   ||||  ||||||||||||||
Db        450 AGGATTCTGGGAAGTGCTCCTG-CCTGAGAGAAAACTCAGCTCAGAAGGAGGAAGGACAG 508

Qy        422 CAGA 425
              ||||
Db        509 CAGA 512


RESULT 4
AZ377232
LOCUS       AZ377232                 588 bp    DNA     linear   GSS 02-OCT-2000
DEFINITION  1M0131P23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0131P23 F, genomic survey sequence.
ACCESSION   AZ377232
VERSION     AZ377232.1  GI:10490932
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 588)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0131  row: P  column: 23
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 588.
FEATURES             Location/Qualifiers
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                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0131P23"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match           15.0%;  Score 71;  DB 8;  Length 588;
  Best Local Similarity   55.2%;  Pred. No. 2.9e-08;
  Matches  234;  Conservative    0;  Mismatches  166;  Indels   24;  Gaps    4;
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```
Qy         23 TTCTAGCCCCCAGAGCCACCTCTGTCACCTTCCTGTTGGGCATCATCCCACCTTCCCAGA 82
              ||| | |   || || || || |||| | |||||| | || |  | | ||||||||||||
Db         98 TTCCAACTGTCACAGACATCTGTGTCCCTTTCCTGATAGGAA--AGCTCACCTTCCCAGA 155

Qy         83 GCCCTGGAGAGCATGGGGAGACCCGGGACCCTGCTGGGTTTCTCTGTCACAAAGGAAAAT 142
              || |||  ||  | | | ||||  ||  | | |||||||| | | |||||||  |  | |
Db        156 GCTCTGAGGACAAAGTGCAGACTGGGACCTCAGCTGGGTCTGTGTGTCACAGGGACACGT 215

Qy        143 AATCCCCCTGGTG----------------TGACAGACCCAAGGACAGAACACAGCAGAGG 186
              |      ||| |                 |||||||| ||      | |  ||||| | |
Db        216 AGGAATGATGGAGGCTCCCTCTTTGATGCTGACAGACTCATATCTGGGAGTCAGCATATG 275

Qy        187 TCAGCACTGGGGAAGACAGGTTGTCCTCCCAGGGGATGGGGGTCCATCCACCTTGCCGAA 246
              ||||| || ||       | |  ||      ||       |   |    || | |
Db        276 TCAGCCCTTGGATGAGTTGTTGTTCTGTGAGGGCATGCCGATGCTTATCAGCCTTGTTGC 335

Qy        247 AAGATTTGTCTGAGGAACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGAGGCAGA 306
              |  | |   |||   |||     ||| || ||||   |||  | |   || ||||
Db        336 TCAAGGTCTTGTTGGAGGAGAATCATAAAGAGAGAAAATGTGAGAAAGATGTGATGCAGC 395

Qy        307 AATGAGAGGGGAGGGGACAGAGGACACCTGAATAAAGA-----CCACACCCATGACCCAC 361
              | |||||| ||| | |||  || |   ||     | | |     |  ||| ||   ||||
Db        396 ACTGAGAGTGGAAGTGACTTAGCAGTTCTATGGACACAGACCCCACCACACACAGCCCAT 455

Qy        362 GTGATGCTGAGAAGTACTCCTGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACAG 421
                ||| ||| ||||| |||||| |||  ||  | |||||| || | ||||||||||||
Db        456 AGGATTCTGGGAAGTGCTCCTG-CCTGAGAGAACACTCAGGTCANAAGGAGGAAGGACAG 514

Qy        422 CAGA 425
                |||
Db        515 TAGA 518
```

RESULT 5
CD709204
LOCUS CD709204 594 bp mRNA linear EST 25-JUN-2003
DEFINITION EST25731 human nasopharynx Homo sapiens cDNA, mRNA sequence.
ACCESSION CD709204
VERSION CD709204.1 GI:32239834
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 594)
AUTHORS Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and
Zeng,Y.-X.
TITLE Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL Unpublished (2003)
COMMENT Contact: YiXin Zeng
Cancer Center
Sun Yat-sen University
651 DongFeng Road East, GuangZhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@gzsums.edu.cn.
FEATURES Location/Qualifiers
source 1. .594
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="normal nasopharynx"
/clone_lib="human nasopharynx"
/note="ESTs generated from a normal nasopharynx cDNA
library from southern Chinese"
ORIGIN

Query Match 15.0%; Score 71; DB 6; Length 594;
Best Local Similarity 100.0%; Pred. No. 2.9e-08;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        401 GGGCAGAGGGAGGAAGGACAGCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCT 460
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 GGGCAGAGGGAGGAAGGACAGCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCT 80

Qy        461 GGAACTCAAGC 471
              ||||||||||||
Db         81 GGAACTCAAGC 91
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RESULT 6
CD708401
LOCUS CD708401 177 bp mRNA linear EST 25-JUN-2003
DEFINITION EST24928 human nasopharynx Homo sapiens cDNA, mRNA sequence.
ACCESSION CD708401
VERSION CD708401.1 GI:32239031
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 177)
AUTHORS Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and
Zeng,Y.-X.
TITLE Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL Unpublished (2003)
COMMENT Contact: YiXin Zeng
Cancer Center
Sun Yat-sen University
651 DongFeng Road East, GuangZhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@gzsums.edu.cn.
FEATURES Location/Qualifiers
source 1. .177
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="normal nasopharynx"
/clone_lib="human nasopharynx"
/note="ESTs generated from a normal nasopharynx cDNA
library from southern Chinese"
ORIGIN

Query Match 14.8%; Score 69.8; DB 6; Length 177;
Best Local Similarity 97.3%; Pred. No. 4.5e-08;
Matches 71; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy        399 CAGGGCAGAGGGAGGAAGGACAGCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTC 458
              | ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CCGGGGAGAGGGAGGAAGGACAGCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTC 62

Qy        459 CTGGAACTCAAGC 471
              |||||||||||||
Db         63 CTGGAACTCAAGC 75
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RESULT 7
CD685182
LOCUS CD685182 338 bp mRNA linear EST 25-JUN-2003
DEFINITION EST1702 human nasopharynx Homo sapiens cDNA, mRNA sequence.
ACCESSION CD685182
VERSION CD685182.1 GI:32200899
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 338)
AUTHORS Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and
Zeng,Y.-X.
TITLE Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL Unpublished (2003)
COMMENT Contact: YiXin Zeng
Cancer Center
Sun Yat-sen University

```
           651 DongFeng Road East, GuangZhou 510060, China
           Tel: 86-1380-9770-743
           Fax: 86-20-8775-4506
           Email: yxzeng@gzsums.edu.cn.
FEATURES             Location/Qualifiers
     source          1. .338
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /tissue_type="normal nasopharynx"
                     /clone_lib="human nasopharynx"
                     /note="ESTs generated from a normal nasopharynx cDNA
                     library from southern Chinese"
ORIGIN

  Query Match             14.8%;  Score 69.8;  DB 6;  Length 338;
  Best Local Similarity   97.3%;  Pred. No. 5.3e-08;
  Matches   71;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        399 CAGGGCAGAGGGAGGAAGGACAGCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTC 458
              | ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 CCGGGGAGAGGGAGGAAGGACAGCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTC 76

Qy        459 CTGGAACTCAAGC 471
              |||||||||||||
Db         77 CTGGAACTCAAGC 89


RESULT 8
CD691155
LOCUS       CD691155                555 bp    mRNA    linear   EST 25-JUN-2003
DEFINITION  EST7678 human nasopharynx Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD691155
VERSION     CD691155.1  GI:32212598
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 555)
  AUTHORS   Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and
            Zeng,Y.-X.
  TITLE     Transcriptional Gene Expression Profile of Human Nasopharynx
  JOURNAL   Unpublished (2003)
COMMENT     Contact: YiXin Zeng
            Cancer Center
            Sun Yat-sen University
            651 DongFeng Road East, GuangZhou 510060, China
            Tel: 86-1380-9770-743
            Fax: 86-20-8775-4506
            Email: yxzeng@gzsums.edu.cn.
FEATURES             Location/Qualifiers
     source          1. .555
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /tissue_type="normal nasopharynx"
                     /clone_lib="human nasopharynx"
                     /note="ESTs generated from a normal nasopharynx cDNA
                     library from southern Chinese"
ORIGIN

  Query Match             14.8%;  Score 69.8;  DB 6;  Length 555;
  Best Local Similarity   97.3%;  Pred. No. 6e-08;
  Matches   71;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        399 CAGGGCAGAGGGAGGAAGGACAGCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTC 458
              | ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 CCGGGGAGAGGGAGGAAGGACAGCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTC 76

Qy        459 CTGGAACTCAAGC 471
              |||||||||||||
Db         77 CTGGAACTCAAGC 89


RESULT 9
AL602851
LOCUS       AL602851                595 bp    mRNA    linear   EST 04-SEP-2003
DEFINITION  DKFZp686P1216_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
            DKFZp686P1216 5', mRNA sequence.
ACCESSION   AL602851
VERSION     AL602851.1  GI:15166357
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 595)
  AUTHORS   Wambutt,R., Heubner,D., Mewes,W., Weil,B. and Wiemann,S.
  TITLE     EST (Wambutt,R., Heubner,D., Mewes,H.W., Weil,B. and Wiemann,S.)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: MIPS
            MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
            This is the 5' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
            sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing
            consortium of the German Genome Project.
            No s1 sequence available.
            This clone (DKFZp686P1216) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES             Location/Qualifiers
     source          1. .595
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="DKFZp686P1216"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="686 (synonym: hlcc3)"
                     /note="Vector: pTriplEx2; Site_1: SfiIA; Site_2: SfiIB;
                     cDNA-collection"
ORIGIN

  Query Match             14.6%;  Score 69;  DB 1;  Length 595;
  Best Local Similarity   100.0%;  Pred. No. 1e-07;
  Matches   69;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        403 GCAGAGGGAGGAAGGACAGCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGG 462
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCAGAGGGAGGAAGGACAGCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGG 60

Qy        463 AACTCAAGC 471
              |||||||||
Db         61 AACTCAAGC 69


RESULT 10
AU140869
LOCUS       AU140869                787 bp    mRNA    linear   EST 05-AUG-2002
DEFINITION  AU140869 PLACE4 Homo sapiens cDNA clone PLACE4000399 5', mRNA
            sequence.
ACCESSION   AU140869
VERSION     AU140869.1  GI:11002390
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 787)
  AUTHORS   Ota,T., Suzuki,Y., Saito,K., Ishii,S., Yamamoto,J., Sugiyama,T.,
            Nishikawa,T., Nakamura,Y., Sugano,S., Masuho,Y. and Isogai,T.
  TITLE     HRI human cDNA project (Ota,T., Suzuki,Y., Saito,K., Ishii,S.,
            Yamamoto,J., Sugiyama,T., Nishikawa,T., Nakamura,Y., Sugano,S.,
```

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            Masuho,Y., Isogai,T.)
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Takao Isogai
            Genomics Laboratory
            Helix Research Institute
            1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
            Tel: 81-438-52-3975
            Fax: 81-438-52-3986
            Email: genomics@hri.co.jp
            HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
            Research Institute; cDNA library construction: Department of
            Virology, Institute of Medical Science, University of Tokyo, and
            Helix Research Institute.
FEATURES             Location/Qualifiers
     source          1. .787
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="PLACE4000399"
                     /tissue_type="placenta"
                     /clone_lib="PLACE4"
                     /note="Vector: pME18SFL3"
ORIGIN

  Query Match             14.6%;  Score 68.8;  DB 1;  Length 787;
  Best Local Similarity   61.9%;  Pred. No. 1.2e-07;
  Matches  130;  Conservative    0;  Mismatches   72;  Indels    8;  Gaps    1;

Qy        262 AACTGAAAATAGAAGGGAAAAAAGAGGAGGGACAAAAGAGGCAGAAATGAGAGGGGAGGG 321
              || || | | |||||||| ||| || || |   ||| |||||| || ||||||||||||
Db          2 AAATGTAGACAGAAGGGAGAAAGGAAGAAGAGAAAATGAGGCAAAACTGAGAGGGGAGGG 61

Qy        322 GACAGAGGACACCTGAATAAAGACCACACCCATGACCCACGTGATGCTGAGAAGTACTCC 381
              |||||||               ||| |    ||         | |||  |||  |||| ||||
Db         62 GACAGAGAGGTGACCTGGGCAGAGCTTCACC--------CATGACCCTGGAAAGTGCTCC 113

Qy        382 TGCCCTAGGAAGAGACTCAGGGCAGAGGGAGGAAGGACAGCAGACCAGACAGTCACAGCA 441
              |||||| ||| ||| |||||    ||  ||||||||||||||| |  |
Db        114 TGCCCTGGGAGGAGGCTCAGCATGGAAAGAGGAAGGACAGCAGAGCCTAAGTCACAGTAG 173

Qy        442 GCCTTGACAAAACGTTCCTGGAACTCAAGC 471
               |||    | | | |||||||| | || ||
Db        174 CCCTGACTACAGCATTCCTGGAGCCCAGGC 203


RESULT 11
CD686649
LOCUS       CD686649                552 bp    mRNA    linear   EST 25-JUN-2003
DEFINITION  EST3170 human nasopharynx Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD686649
VERSION     CD686649.1  GI:32203762
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 552)
  AUTHORS   Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and
            Zeng,Y.-X.
  TITLE     Transcriptional Gene Expression Profile of Human Nasopharynx
  JOURNAL   Unpublished (2003)
COMMENT     Contact: YiXin Zeng
            Cancer Center
            Sun Yat-sen University
            651 DongFeng Road East, GuangZhou 510060, China
            Tel: 86-1380-9770-743
            Fax: 86-20-8775-4506
            Email: yxzeng@gzsums.edu.cn.
FEATURES             Location/Qualifiers
     source          1. .552
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /tissue_type="normal nasopharynx"
                     /clone_lib="human nasopharynx"
                     /note="ESTs generated from a normal nasopharynx cDNA
                     library from southern Chinese"
ORIGIN

  Query Match             14.3%;  Score 67.6;  DB 6;  Length 552;
  Best Local Similarity   94.6%;  Pred. No. 2.4e-07;
  Matches   70;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        398 TCAGGGCAGAGGGAGGAAGGACAGCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTT 457
              | | ||| | ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         11 TTATGGCCGGGGGAGGAAGGACAGCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTT 70

Qy        458 CCTGGAACTCAAGC 471
              ||||||||||||||
Db         71 CCTGGAACTCAAGC 84


RESULT 12
BM829043
LOCUS       BM829043                220 bp    mRNA    linear   EST 06-MAR-2002
DEFINITION  K-EST0101950 S9SNU601 Homo sapiens cDNA clone S9SNU601-52-B11 5',
            mRNA sequence.
ACCESSION   BM829043
VERSION     BM829043.1  GI:19185452
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 220)
  AUTHORS   Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
            Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
            Kim,Y.S.
  TITLE     21C Frontier Korean EST Project 2001
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4470
            Fax: +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
            Plate: 52  row: B  column: 11
            High quality sequence stop: 220.
FEATURES             Location/Qualifiers
     source          1. .220
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="S9SNU601-52-B11"
                     /sex="M"
                     /tissue_type="Ascites"
                     /cell_type="Epithelial"
                     /cell_line="SNU-601"
                     /lab_host="Top10F'"
                     /clone_lib="S9SNU601"
                     /note="Organ: Stomach; Vector: pME18-FL3; Site_1: XhoI;
                     Site_2: XhoI; The poly (A)+ RNA was dephosphorylated with
                     bacterial alkaline phosphatase (BAP) and then decapped
                     with tabacco acid pyrophosphatase (TAP). The decapped
                     intact mRNA was ligated with DNA-RNA linker including SfiI
                     site by treatment of T4 RNA ligase and the first strand
                     cDNA was synthesized with Superscript II using SfiI
                     oligo-dT primer. After first strand synthesis, RNA was
                     degraded by NaOH treatment and cDNA was amplified by PCR
                     reaction. The PCR products were digested with SfiI and
                     cloned into DraIII- digested pME18S-FL3 vector. The
                     obtained cDNA vectors were used for transformation of
                     competent cells E. coli Top10F' by electroporation method.
                     The cDNA libraries constructed by this method are
                     full-length enriched cDNA library."
```

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ORIGIN

  Query Match           14.2%;  Score 67;  DB 4;  Length 220;
  Best Local Similarity  100.0%;  Pred. No. 2.8e-07;
  Matches   67;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        405 AGAGGGAGGAAGGACAGCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAA 464
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGAGGGAGGAAGGACAGCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAA 60

Qy        465 CTCAAGC 471
              |||||||
Db         61 CTCAAGC 67


RESULT 13
BM836430
LOCUS       BM836430                275 bp    mRNA    linear   EST 06-MAR-2002
DEFINITION  K-EST0112089 S9SNU601 Homo sapiens cDNA clone S9SNU601-61-B06 5',
            mRNA sequence.
ACCESSION   BM836430
VERSION     BM836430.1  GI:19192839
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 275)
  AUTHORS   Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
            Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
            Kim,Y.S.
  TITLE     21C Frontier Korean EST Project 2001
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4470
            Fax: +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
            Plate: 61  row: B  column: 06
            High quality sequence stop: 275.
FEATURES             Location/Qualifiers
     source          1. .275
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="S9SNU601-61-B06"
                     /sex="M"
                     /tissue_type="Ascites"
                     /cell_type="Epithelial"
                     /cell_line="SNU-601"
                     /lab_host="Top10F'"
                     /clone_lib="S9SNU601"
                     /note="Organ: Stomach; Vector: pME18-FL3; Site_1: XhoI;
                     Site_2: XhoI; The poly (A)+ RNA was dephosphorylated with
                     bacterial alkaline phosphatase (BAP) and then decapped
                     with tabacco acid pyrophosphatase (TAP). The decapped
                     intact mRNA was ligated with DNA-RNA linker including SfiI
                     site by treatment of T4 RNA ligase and the first strand
                     cDNA was synthesized with Superscript II using SfiI
                     oligo-dT primer. After first strand synthesis, RNA was
                     degraded by NaOH treatment and cDNA was amplified by PCR
                     reaction. The PCR products were digested with SfiI and
                     cloned into DraIII- digested pME18S-FL3 vector. The
                     obtained cDNA vectors were used for transformation of
                     competent cells E. coli Top10F' by electroporation method.
                     The cDNA libraries constructed by this method are
                     full-length enriched cDNA library."
ORIGIN

  Query Match           14.2%;  Score 67;  DB 4;  Length 275;
  Best Local Similarity  100.0%;  Pred. No. 2.9e-07;
  Matches   67;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        405 AGAGGGAGGAAGGACAGCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAA 464
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGAGGGAGGAAGGACAGCAGACCAGACAGTCACAGCAGCCTTGACAAAACGTTCCTGGAA 60

Qy        465 CTCAAGC 471
              |||||||
Db         61 CTCAAGC 67


RESULT 14
BM752482
LOCUS       BM752482                279 bp    mRNA    linear   EST 04-MAR-2002
DEFINITION  K-EST0029023 S9SNU601 Homo sapiens cDNA clone S9SNU601-6-B10 5',
            mRNA sequence.
ACCESSION   BM752482
VERSION     BM752482.1  GI:19082100
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 279)
  AUTHORS   Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
            Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
            Kim,Y.S.
  TITLE     21C Frontier Korean EST Project 2001
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4470
            Fax: +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
            Plate: 6  row: B  column: 10
            High quality sequence stop: 279.
FEATURES             Location/Qualifiers
     source          1. .279
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
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                     Site_2: XhoI; The poly (A)+ RNA was dephosphorylated with
                     bacterial alkaline phosphatase (BAP) and then decapped
                     with tabacco acid pyrophosphatase (TAP). The decapped
                     intact mRNA was ligated with DNA-RNA linker including SfiI
                     site by treatment of T4 RNA ligase and the first strand
                     cDNA was synthesized with Superscript II using SfiI
                     oligo-dT primer. After first strand synthesis, RNA was
                     degraded by NaOH treatment and cDNA was amplified by PCR
                     reaction. The PCR products were digested with SfiI and
                     cloned into DraIII- digested pME18S-FL3 vector. The
                     obtained cDNA vectors were used for transformation of
                     competent cells E. coli Top10F' by electroporation method.
                     The cDNA libraries constructed by this method are
                     full-length enriched cDNA library."
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KEYWORDS    EST.
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REFERENCE   1  (bases 1 to 355)
  AUTHORS   Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
            Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
            Kim,Y.S.
  TITLE     21C Frontier Korean EST Project 2001
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4470
            Fax: +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
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                     Site_2: XhoI; The poly (A)+ RNA was dephosphorylated with
                     bacterial alkaline phosphatase (BAP) and then decapped
                     with tabacco acid pyrophosphatase (TAP). The decapped
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                     obtained cDNA vectors were used for transformation of
                     competent cells E. coli Top10F' by electroporation method.
                     The cDNA libraries constructed by this method are
                     full-length enriched cDNA library."
ORIGIN

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